

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

Om nucleic - nucleic search, using sw model
 Run on: December 10, 2005, 23:23:15 ; Search time 241 Seconds
 (without alignments)
 159.148 Million cell updates/sec

Title: US-10-031-158B-13
 Perfect score:
 Sequence: 1 gggcaaggttgggaaaa.....atttaaaaaatgaaagt 1027

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA_New/*

1: /cggn2_6_ptodata/2/pubpna/US09_NEW_PUB.seq;*
 2: /cggn2_6_ptodata/2/pubpna/US06_NEW_PUB.seq;*
 3: /cggn2_6_ptodata/2/pubpna/US07_NEW_PUB.seq;*
 4: /cggn2_6_ptodata/2/pubpna/US08_NEW_PUB.seq;*
 5: /cggn2_6_ptodata/2/pubpna/PCTC NEW PUB.seq;*
 6: /cggn2_6_ptodata/2/pubpna/US10_NEW_PUB.seq;*
 7: /cggn2_6_ptodata/2/pubpna/US11_NEW_PUB.seq;*
 8: /cggn2_6_ptodata/2/pubpna/US11_NEW_PUB.seq;*
 9: /cggn2_6_ptodata/2/pubpna/US60_NEW_PUB.seq;*
 10: /cggn2_6_ptodata/2/pubpna/US60_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	35.8	3.6	600	US-10-750-185-1996
C 2	34.6	3.4	1561	US-10-750-185-40906
C 3	34	3.3	905	US-10-750-185-53770
C 4	34	3.3	1173	US-10-750-185-52322
C 5	34	3.3	170837	US-11-121-086-97
C 6	34	3.3	191797	US-11-121-086-13
C 7	33.8	3.3	96988	US-11-17-17-196
C 8	33.6	3.3	182303	US-11-121-086-45
C 9	33.4	3.3	1515	US-10-750-185-40420
C 10	33.4	3.3	1567	US-10-750-185-25199
C 11	33.2	3.2	40439	US-10-993-509-1
C 12	33	3.2	1128	US-10-750-185-54062
C 13	33	3.2	108214	US-11-17-17-211
C 14	32.8	3.2	600	US-10-750-185-102
C 15	32.8	3.2	1037	US-10-518-753-14
C 16	32.8	3.2	1449	US-10-750-185-53517
C 17	32.8	3.2	2767	US-10-750-185-24844
C 18	32.8	3.2	4497	US-10-518-753-15
C 19	32.8	3.2	162173	US-11-121-086-75
C 20	32.4	3.2	161874	US-11-121-086-75
C 21	32.2	3.1	600	US-10-750-185-20145
C 22	32.2	3.1	944	US-10-750-185-39148
C 23	32.2	3.1	2069	US-10-750-185-49897

ALIGNMENTS

```

RESULT 1
US-10-750-185-1996/c
; Sequence 1995, Appl. Publ. Information No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMi GENOMICS, INC.
; APPLICANT: DENISE, SUE K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: RANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMi1100-2
; CURRENT APPLICATION NUMBER: US/10/750-185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1996
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT18519
US-10-750-185-1996
Query Match Best Local Similarity 52.0%; Pred. No. 0.17; Mismatches 97; Indels 1; Gaps 1; Matches 106; Conservative 0; Score 36.8; DB 6; Length 600;
QY 163 GAGAATTTCCGTAGTTAAGTACATGGCAGANAGAGACACGTT 222
Db 528 GATGATTTCAGCTTAACTGTAACGCTTCCTGTT 469
QY 223 CTGGATCCAGGAGAACCTGAGACTAACGACATACATGAAATTAGCTTG 282
Db 468 ATCAGTGTCTTAAAGGAAATCATACACACACATCAACCCACGATCTATGGCA 409
QY 283 TTA-ACGGTGCCTGAAGTCACTGGCAAGACAGATGATCGCAGACATGAGAA 341
Db 408 TTATTCCTTAGGATAAACATAAGTTAAAGAAAGAAAGTGTGTTAGGAGAA 349

```

RESULT 2
US-10-750-185-40906/c
; Sequence 40906, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMIL100-2
; CURRENT APPLICATION NUMBER: US 10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 40906
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Bovine 19866881662064
; US-10-750-185-40906

[REDACTED] Query Match 3.4%; Score 34; DB 6; Length 1561;
Query Local Similarity 61.8%; Pred. No. 1.5; Mismatches 55; Conservative 0; Indels 0; Gaps 0;
Matches 55; Conservatve 0; Mismatches 34; Indels 0; Gaps 0;

Qy 655 TTGGCTTCTTCCTCGGTTGGCCATTCAGTCTCATGTGTAACATCATT 714
Db 1426 TTTGGCCATGTCACATGGCATGTGGATCTAGTTCCTCTGGTGTATTAACTACAGG 1367

Qy 715 ATGGATAACGGTTTCAAACAGTGCGG 743
Db 1366 TGTATCTGACTCTTGGATCTGGGC 1338

RESULT 3
US-10-750-185-53770
; Sequence 53770, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMIL100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 53770
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Bovine 19866880693972
; US-10-750-185-53770

Query Match 3.3%; Score 34; DB 6; Length 905;
Best Local Similarity 50.0%; Pred. No. 1.6; Mismatches 85; Conservative 0; Indels 0; Gaps 0;

Qy 855 ATAGTGATGAGATCCCTCGGCGCTTCAGCTCTCTCTAGTGTCTTAATCAGAT 914
Db 456 ATAGTCTAGACATCATCAAGCTGCTGAGGCTCTCACGGTCATATGATGA 515

RESULT 4
US-10-750-185-52322/c
; Sequence 52322, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMIL100-2
; CURRENT APPLICATION NUMBER: US 10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 52322
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Bovine 198668806907657
; US-10-750-185-52322

Query Match 3.3%; Score 34; DB 6; Length 1173;
Best Local Similarity 66.2%; Pred. No. 1.9; Mismatches 49; Conservative 0; Indels 0; Gaps 0;

Qy 953 AGTCCTCTTGTAGTTGAATTATGTCGGTGGTGTCTCGTAATAAGAAATAATTAA 1012
Db 231 ATTAGTATTTACTAGTTGAATATGTTAGTGTAGTGTAGTGTAGTGTCTATAACAAATATTAA 172

Qy 1013 AAAAATGAAAGT 1026
Db 171 CCAAAAATAAAGT 158

RESULT 5
US-11-121-086-97/c
; Sequence 97, Application US/11121086
; Publication No. US2005026459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NILSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09118.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 97
; LENGTH: 170837
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-97

Query Match 3.3%; Score 34; DB 7; Length 170837;
Best Local Similarity 52.1%; Pred. No. 40; Mismatches 76; Conservative 0; Indels 0; Gaps 0;

Qy

Db

Qy

RESULT 6
US-11-121-086-13/c
; Sequence 13, Application US/11121086
; Publication No. US200502664591
; GENERAL INFORMATION:
; APPLICANT: POUlsen, TIM S.
; INVENTOR: NIESEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEAR ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121, 086
; PRIOR FILING DATE: 2005-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 13
; LENGTH: 191797
; ORGANISM: Homo sapiens
; US-11-121-086-13

Query Match 3.3%; Score 34; DB 7; Length 191797;
Best Local Similarity 51.3%; Pred. No. 43; Mismatches 0; Indels 0; Gaps 0;
Matches 79; Conservative 0; Gaps 0;

Qy 311 AGAACACAGATGATCTGCAGCATGGATAATAAACCGAGTGTACAGAAATTA 370
Db 57371 AAAAACACAAATGGCAAGATTGAACTCAAGGAGATATAAATG 57312
Qy 371 TCTTTCCCTCCAATAAGAGCAGGATGTCATCACATTGGATCCAAAGACATTGTCAAAG 430
Db 57311 TGTAAATTATGTAACACATGTAATTCTCATCAATAAGAGAAATGCCAATTA 57252
Qy 431 ATGCAAATGATCACTATGTCAGTCACAA 464
Db 57251 ATTACAATAAACGTCATTTCACCCATCAA 57218

RESULT 7
US-11-117-187-196
; Sequence 196, Application US/1111187
; Publication No. US200502665601
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; INVENTOR: COHENHARV, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117, 187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531, 120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125, 219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 196
; LENGTH: 96988
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

Query Match 3.3%; Score 33.8; DB 7; Length 96988;
Best Local Similarity 45.6%; Pred. No. 33; Mismatches 142; Indels 0; Gaps 0;
Matches 119; Conservative 0;

Qy 179 ATGTTATTAGATACATTGGCAGAAGAGAGAACAGATCTGGATCCAGGG 238
Db 44761 ATGTAGTAGTGTGATATCAGGATACACTCAAGATGTCGAAGAAATTCAGAAAG 44820
Qy 239 GAAACACCATGAGACTACAGACACATACATGAAATTAGCTGGTAAAGGTGCCAGAA 298
Db 44821 AGTGACGGAGGTTGGAGATGCCAGCATGATGCTTACTACCTTGGAATG 44880
Qy 299 AGTCACTGAGCAAGAACAGATGATGATGTCAGATGAGATAATAAACGGAGTG 358
Db 44881 AAGTAACACAGAGAGATGGATTTCTACTCAGAAGCGATGCTAGGAACAC 44940
Qy 359 ATCAGAGAAATRACTCTCCATAAAGACCGATGTCATCACAAUTGGATCCAAGAGCA 418
Db 44941 TPAAAAGTTAGATGAAATFACTCAACCCGGTAGACACCAATGGAATCGGAAATCA 45000
Qy 419 ATGTCACAAAGATGCAATG 439
Db 45001 ATTATCAGAAAGAAAGAAAG 45021

RESULT 8
US-11-121-086-45/c
; Sequence 45, Application US/11121086
; Publication No. US200502664591
; GENERAL INFORMATION:
; APPLICANT: POUlsen, TIM S.
; INVENTOR: NIESEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEAR ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121, 086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567, 570
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 45
; LENGTH: 182303
; ORGANISM: Homo sapiens
; US-11-121-086-45

Query Match 3.3%; Score 33.6; DB 7; Length 182303;
Best Local Similarity 48.4%; Pred. No. 55; Mismatches 99; Indels 0; Gaps 0;
Matches 93; Conservative 0;

Qy 17 AAAAATCAGGATTGGTCGGAACAAAGCTTATCATAAGATAAACACTGATG 76
Db 45288 AAAATGAGAAGATTCTCCACATGATACCTCTTCCTCCACTATTTGTCATTCCTG 45229
Qy 77 CAGATGTTCCCTCCAGCCCACTATTCTCTCTCAATGCTGAAACAAAGCTCAGA 136
Db 45228 TTGATGATCCAAAGCCACTTAATCCATGCTCAGATGATTACGCCAGAGG 45169
Qy 137 AGCTGGACATACCTTGTCTCTGAGAAATTTCCTGATGTTAGATCATT 196
Db 45168 AGACCCATATAGCGATPATCATTTATACCTTATTCACCCACAAATCAATAATG 45109
Qy 197 GCGAAGAGAAGA 208
Db 45108 TGTGATGAAAGA 45097

RESULT 9
US-10-750-185-40420
; Sequence 40420, Application US/10750185
; Publication No. US20050260603A1

; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMII110-2
; CURRENT APPLICATION NUMBER: US10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 40420
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Bovine 19866881526906
; US-10-750-185-40420

Query Match Best Local Similarity 3.3%; Score 33.4; DB 6; Length 1515; Matches 106; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 25 AGAGTTGGCCCGGAAACAAGCTTATCATACAGATAAACACTGATGAGATGT 84
Db 23 AAATCAGTTATCCAGCAAAATAGTATRACTTAGTCAGAGGACAAACCTT 82
QY 85 TCCCCCAAAGCCACTATTTCCTCTTCAATTGTGAGAACAGCTTCAAGGTGA 144
Db 83 TCTCTAGAAAGACTCTGAAACACTGCTCTGCTCTTAGGAACTCTGACAGGACTT 142
Qy 145 ACATACCTTGTCCTGTGAGAATTTCCTGTGATGTTAAAGATACATGGCAAGA 204
Db 143 ACATGAATCATTCATTTGTAATACAAATTCTGTGAGCAGCGTTAGCTGCCAGT 202
Qy 205 AGAGAGGACACACGATTCGGATCCAGGAGGGACACCATGAA 251
Db 203 TGGATTTAGAACAGATCAGCATTAATGGATGGACACAGGATGAA 249

RESULT 10
US-10-750-185-25199/C
; Sequence 25199, Application US/10750185
; Publication No. US2005026003A1

; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMII110-2
; CURRENT APPLICATION NUMBER: US10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 1
; LENGTH: 40439
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2402)..(2402)
; OTHER INFORMATION: n is 'c' or 'g'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2722)..(2722)
; OTHER INFORMATION: n is 'c' or 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2799)..(2799)
; OTHER INFORMATION: n is 'g' or 'a'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3799)..(3898)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6337)..(6436)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1129)..(1182)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1405)..(1504)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'

QY 283 TTACGGGCCGAAACTGACGACAAAGAACAGATGATGCTGAGACTGAGAT 342
Db 582 TTATGCTTGAGGATATTTATTAGAGCACACATGCATGACTGTAATT 523
Qy 343 AATAAACGGAGTGTGCAAGAATTCTTCTCCATAAGACCGATGTCATCA 402
Db 522 TATCTCAAATGAGAGTATCTGAGAAATAGTAGCAGCATAATGACCTATG 463
Qy 403 ATGGATCCAAAGACAACTGTCAGAAAGATGCAATGACTACTGTCAGCTCA 462
Db 462 CAATGGCUCAGGATCATCTGCAACATGACAGATATCTAAGGACATGAA 403
Qy 463 AACACCTTGATATTAGTGA 485
Db 402 AATTTTTCTTATTTAGTTGAA 380

RESULT 11
US-10-993-503-1
; Sequence 1, Application US/10993509
; Publication No. US20050250121A1

; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasiou, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Dain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Ural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: Disease
; FILE REFERENCE: 2300_0050001
; CURRENT APPLICATION NUMBER: US10/993,509
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: US 60/524,637
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1
; LENGTH: 40439
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2402)..(2402)
; OTHER INFORMATION: n is 'c' or 'g'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2722)..(2722)
; OTHER INFORMATION: n is 'c' or 't'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2799)..(2799)
; OTHER INFORMATION: n is 'g' or 'a'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3799)..(3898)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6337)..(6436)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1129)..(1182)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'

QY 283 TTACGGGCCGAAACTGACGACAAAGAACAGATGATGCTGAGACTGAGAT 342
Db 582 TTATGCTTGAGGATATTTATTAGAGCACACATGCATGACTGTAATT 523
Qy 343 AATAAACGGAGTGTGCAAGAATTCTTCTCCATAAGACCGATGTCATCA 402
Db 522 TATCTCAAATGAGAGTATCTGAGAAATAGTAGCAGCATAATGACCTATG 463
Qy 403 ATGGATCCAAAGACAACTGTCAGAAAGATGCAATGACTACTGTCAGCTCA 462
Db 462 CAATGGCUCAGGATCATCTGCAACATGACAGATATCTAAGGACATGAA 403
Qy 463 AACACCTTGATATTAGTGA 485
Db 402 AATTTTTCTTATTTAGTTGAA 380

NAME/KEY: misc feature
; LOCATION: (11523)..(11622)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19842)..(19941)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22316)..(22415)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (27030)..(27129)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (29535)..(29634)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31929)..(32028)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (34403)..(34502)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (36929)..(37028)
; OTHER INFORMATION: n is 'a', 't', 'g', or 'c'
; US-10-993-509-1

Query Match
Best Local Similarity 3.2%; Score 33.2; DB 6; Length 40439;
Matches 116; Conservative 0; Mismatches 218; Indels 2; Gaps 1;

Qy 485 ACTCTCCCTCTGCTCCAGAGTGTCAACTGATCTCCACCTCCTCGTTA 544
Db 34298 ATCTGCAACTCTCCGCTCCAGAGTGTCAACTGATCTCCACCTCCTCGTAGCTG 34357

Qy 545 GAGAACGGCTCTGCTGCAATGGAGAAATCATACAGAGGGTGACAGAGGG 604
Db 34358 GATTAACAGGGCTGTGCACATTGTCTGTAAT-TTCAATTTTNNNNNNNNNN 34415

Qy 605 ATCTTTCTCATCGGTTATTGTCCTAGAACGGCTCTGAGGGATCTGGCTTC 664
Db 34416 NNN 34475

Qy 665 TTTCTGCGTTTGGCCATTCTGCTCATGGTGACTATCTATATGATAAC 724
Db 34476 NNNNNNNNNNNNNNNNNNNNNNNNATTATGAGAACATCTATATTATCTAG 34535

Qy 725 GGTTCAACACAGTGCCACAGAGAACCTACTCTGTAATACATGGGAATGCC 784
Db 34536 TGTTCAACACAGTGCCACAGAGAACCTACTCTGTAATACATGGGAATGCC 34595

Qy 785 ACGGGGATCTCCGACCAATCTCCATGTTCC 820
Db 34596 AGGGCAGAGCCGACAGCAACCCGCTTATTC 34631

RESULT 13
US-11-117-187-211
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREBUSS, DAPHNE
; APPLICANT: COOPENHAVEN, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIORITY APPLICATION NUMBER: US/09/531,120
; PRIORITY FILING DATE: 2000-03-17
; PRIORITY APPLICATION NUMBER: 60/125,219
; PRIORITY FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211
Query Match
Best Local Similarity 3.2%; Score 33; DB 7; Length 1082144;
Matches 150; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

Qy 159 TCTTGAGAAATTTCCTGGTGTATAGTGTATTTATACCAAAATAATTAAC 493387
Db 493328 TAATTAATAATTAGTGTATTTATACCAAAATAATTAAC 493387

Qy 219 GATTCTGGATCCAGGGGACACCATGAGACTACAGACACATACAGAATTG 278
Db 493388 AATATCTGAAATACCTGTATTCGAAATTGTGTATTTATATPAC 493447

Qy 279 CTGGTAAAGGGGCCAGAACAGTCACTGAGAACAGATGTATGTCAGACATGA 338

RESULT 12
US-10-750-185-54062
; Sequence 54062, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMi GENOMICS, INC.
; APPLICANT: DENISE, Sue K.

```

Query Match 3.24; Score 32.8; DB 6; Length 600;
Best Local Similarity 59.8%; Pred. No. 2, 9; Mismatches 37; Indels 0; Gaps 0;

QY 18 AAAATCAGGATTGTCGCCGACAACTTACATACGATAAACACTGTATGC 77
Db 193 AAAAATGAAATATGAGATCCCTGTCAGATTTAAGATTTCAAGAAGTGAAGC 134
QY 78 AGATGTTCCCCAACGCCACTATTTCCTTC 109
Db 133 AGATGTTTACACCAAGCACAGGCCTTCIGC 102

RESULT 15
US-10-518-753-14
; Sequence 14, Application US/10518753
; Publication No. US20050262589A1
; GENERAL INFORMATION:
; APPLICANT: Calgene LLC
; TITLE OF INVENTION: Nucleic Acid Sequences and Methods of Use for the Production of Fatty Acids
; FILE REFERENCE: 16518.129
; CURRENT APPLICATION NUMBER: US/10/518,753
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Glycine max
US-10-518-753-14

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 10, 2005, 22:15:03 ; Search time 890 Seconds
(without alignments)
9542.305 Million cell updates/sec

Title: US-10-031-158B-13
Perfect Score: 1027
Sequence: 1. gggcaaggttggcaaaaa.....atttaaaaaatgaaagg 1027

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq: *
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq: *
4: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq: *
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq: *
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq: *
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq: *
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq: *
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	1027	100.0	1027	5	US-10-205-823-404	Sequence 404, APP
2	1027	100.0	1027	9	US-10-756-149-2859	Sequence 2859, APP
3	1027	100.0	1027	10	US-10-11-051-454-404	Sequence 404, APP
4	1013.8	98.7	1039	8	US-10-543-795A-23	Sequence 23, APP
5	1013.8	98.7	1395	9	US-10-948-518-23	Sequence 23, APP
6	968.2	94.3	1799	6	US-10-101-510-492	Sequence 492, APP
7	945.6	92.1	1418	3	US-09-957-701-49	Sequence 16, APP
8	906	88.2	1155	3	US-09-925-300-58	Sequence 58, APP
9	902.2	87.8	1421	3	US-03-954-456-317	Sequence 317, APP
10	902.2	87.8	1421	9	US-10-843-641A-3344	Sequence 334, APP
11	838	81.6	1586	3	US-03-960-706-676	Sequence 676, APP
12	838	81.6	1586	3	US-03-873-319-424	Sequence 424, APP
13	81.6	1586	3	US-10-847-918-14	Sequence 14, APP	
14	795.8	77.5	1162	8	US-10-357-930-21517	Sequence 21517, APP
15	795.8	77.5	1162	8	US-10-357-930-24142	Sequence 24142, APP
16	795.8	77.5	1162	8	US-10-357-930-24529	Sequence 24529, APP
17	795.8	77.5	1162	8	US-10-357-930-24533	Sequence 24533, APP
18	795.8	77.5	1162	8	US-10-357-930-24840	Sequence 24840, APP
19	795.8	77.5	1162	8	US-10-357-930-27359	Sequence 27359, APP
20	795.8	77.5	1162	8	US-10-357-930-27740	Sequence 27740, APP
21	795.8	77.5	1162	8	US-10-357-930-27740	Sequence 27740, APP
22	619	60.3	924	8	US-10-357-930-25081	Sequence 25081, APP
23	589	US-10-737-082-97	9	US-10-737-082-97	Sequence 97, APP	

ALIGNMENTS

RESULT 1
US-10-205-823-404
; Sequence 404, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endge, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Belia
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF PROSTATE CANCER
FILE REFERENCE: MRE-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIORITY APPLICATION NUMBER: 60/3307, 982
PRIORITY FILING DATE: 2001-07-25
PRIORITY APPLICATION NUMBER: 60/314, 356
PRIORITY FILING DATE: 2001-08-22
PRIORITY APPLICATION NUMBER: 60/325, 020
PRIORITY FILING DATE: 2001-09-25
PRIORITY APPLICATION NUMBER: 60/341, 746
PRIORITY FILING DATE: 2001-12-12
PRIORITY APPLICATION NUMBER: 60/362, 158
PRIORITY FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 404
LENGTH: 1027
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-404

Query Match 100.0%; Score 1027; DB 5; Length 1027;
Best Local Similarity 100.0%; Pred. No. 1.le-233;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGSCAGACTGG3CAAAATCAGGATTCTCCCGAACACTTATCATTCAC 60

Db	1	GGGAAAGAGTGGCCAAAAATCAAGGTTTGGTCGGACAAAGCTATCATACA	60
Qy	61	GATAAACAACTGTGATCAGATTCCCCAAGCCACTATTTCTCCTCAATRGCT	120
Db	61	GATAAACAACTGTGATCAGATTCCCCAAGCCACTATTTCTCCTCAATRGCT	120
Qy	121	GAACAACTCCAGAAAGCTCGAACATACCTTGTCTCTGAGAAATTTCCTGAT	180
Db	121	GAACAACTCCAGAAAGCTCGAACATACCTTGTCTCTGAGAAATTTCCTGAT	180
Qy	181	GTATTAGATACATGGCAAGAAAGAGAGAACAGATCTGGGATCCAGGGGG	240
Db	181	GTATTAGATACATGGCAAGAAAGAGAGAACAGATCTGGGATCCAGGGGG	240
Qy	241	AACACATGAGACTAACGACATACATGAATTAGCTGGTTACCGTGCAGAAG	300
Db	241	AACACATGAGACTAACGACATACATGAATTAGCTGGTTACCGTGCAGAAG	300
Qy	301	TCACTGACAAGAACAGAGTATCTCAGACATAGAAATTAGCTGGTTACCGAGTGAT	360
Db	301	TCACTGACAAGAACAGAGTATCTCAGACATAGAAATTAGCTGGTTACCGAGTGAT	360
Qy	361	CAAGAAATTATCTTCTCCAAATAAGAGGATGTCACATCACATGATCCAAAGACAT	420
Db	361	CAAGAAATTATCTTCTCCAAATAAGAGGATGTCACATCACATGATCCAAAGACAT	420
Qy	421	TGTCAGATGCAATGATACACTACTGTCAGCTACACACACCTCTGATATTAC	480
Db	421	TGTCAGATGCAATGATACACTACTGTCAGCTACACACACCTCTGATATTAC	480
Qy	481	ATGTAACCTCTCTCTAGAGCTGCTTATTCACCTGCTGCTGAGCTACACACCTCTG	540
Db	481	ATGTAACCTCTCTCTAGAGCTGCTTATTCACCTGCTGCTGAGCTACACACCTCTG	540
Qy	541	CITAGAAGACGCCCTTGCTCGATGAGAGAAATCATACAGACGGGACAAAGGA	600
Db	541	CITAGAAGACGCCCTTGCTCGATGAGAGAAATCATACAGACGGGACAAAGGA	600
Qy	601	GGCCATCTTCTCATCGGTTATGTCCTAGAGCTCTCTGAGATGTTGGC	660
Db	601	GGCCATCTTCTCATCGGTTATGTCCTAGAGCTCTCTGAGATGTTGGC	660
Qy	661	TTCTCTCTGGGATTGGCCATTTCAGTCTGACTATCTCATTTGTT	720
Db	661	TTCTCTCTGGGATTGGCCATTTCAGTCTGACTATCTCATTTGTT	720
Qy	721	TAACGTTTCAACACTGGGACACAGAGAACCTCTCTGATAACATGAGGAAT	780
Db	721	TAACGTTTCAACACTGGGACACAGAGAACCTCTCTGATAACATGAGGAAT	780
Qy	781	AGCCACGGGATCTCAGCACCATTCTCCATGTTTCCACAGCTCCAGCCAAACC	840
Db	781	AGCCACGGGATCTCAGCACCATTCTCCATGTTTCCACAGCTCCAGCCAAACC	840
Qy	841	AAATAGCCCTCTTGTGAGACATCTGGCTCTGCTGCTGTTAGGAT	900
Db	841	AAATAGCCCTCTTGTGAGACATCTGGCTCTGCTGCTGTTAGGAT	900
Qy	901	TCTTTAATCAGATACTGCCCTGAGCTTCATTACACCCCTGAGCGTCTCT	960
Db	901	TCTTTAATCAGATACTGCCCTGAGCTTCATTACACCCCTGAGCGTCTCT	960
Qy	961	TGCTTAGTGAATTAGTGGTGTGTTTCCGAAATAAATTAATAAATG	1020
Db	961	TGCTTAGTGAATTAGTGGTGTGTTTCCGAAATAAATTAATAAATG	1020
Qy	1021	AAAAGTT 1027	
Db	1021	AAAAGTT 1027	
Qy	721	TACGGTTTCAACCAGTGGCACAGAGAACCTCTGTPATAACATGAGAAT	780

RESULT 3

US-11-051-454-404

; Sequence 404, Application US/105,454

; Publication No. US20050191673A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Monahan, John E.

; APPLICANT: Endge, Wilson O.

; APPLICANT: Gannavarapu, Manjula

; APPLICANT: Gorbatcheva, Bella

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Kamatkar, Shubhangi

; APPLICANT: Wonsley, Angela M.

; APPLICANT: Glatt, Karen

; APPLICANT: Zhao, Xumei

; APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/11/051,454

CURRENT FILING DATE: 2005-02-04

PRIOR APPLICATION NUMBER: US/10/205,823

PRIOR FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325,020

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/341,746

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362,158

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FALSEQ for Windows Version 4.0

SEQ ID NO 404

LENGTH: 1027

TYPE: DNA

ORGANISM: Homo sapiens

US-11-051-454-404

Query Match Best Local Similarity 100.0%; Score 1027; DB 10; Length 1027; Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCGAGAGCTTGGCAAAATGCAAGTTATTGTGCCGGAACAGCTTATCATTACA 60

Db 1 GGGCAAGAGTTGGCAAAATGCAAGTTATTGTGCCGGAACAGCTTATCATTACA 60

QY 61 GATAAACACTTGATGAGTTCCCAAGCCACTATTTCTTCATGCT 120

Db 61 GATAAACACTTGATGAGTTCCCAAGCCACTATTTCTTCATGCT 120

QY 121 GAACAAAGCTCCAGAAGGCTGACATACCTTGCTCTGAGAAATTTCCTGAT 180

Db 121 GAACAAAGCTCCAGAAGGCTGACATACCTTGCTCTGAGAAATTTCCTGAT 180

QY 181 GTTATTAGATACATGGCAAGAAAGAGCAACAGATCTGGGATCCAGGGGG 240

Db 181 GTTATTAGATACATGGCAAGAAAGAGCAACAGATCTGGGATCCAGGGGG 240

QY 901 TTCTTAATCAGATACTGCTGAGCTTCTAGCTTGCCCTCTCTTAGTG 900

Db 901 TTCTTAATCAGATACTGCTGAGCTTCTAGCTTGCCCTCTCTTAGTG 900

QY 960 TTCTTAGTGAATTATGGGGTTTCCCTAAAGCAAAATAATTAAAAATG 1020

Db 960 TTCTTAGTGAATTATGGGGTTTCCCTAAAGCAAAATAATTAAAAATG 1020

QY 1021 AAAGTT 1027

Db 1021 AAAGTT 1027

QY 1021 AAAGTT 1027

Db 1021 AAAGTT 1027

QY 361 CAGAAATTATCTTCCCAAATAAGCAAGGGATCATCACATGGATCCAAAGCAT 420

Db 361 CAGAAATTATCTTCCCAAATAAGCAAGGGATCATCACATGGATCCAAAGCAT 420

QY 421 TTGTCAAAGATGCAATGAGTACACTACTGGCTGAGCTCACAAACCTCTGCATATAC 480

Db 421 TTGTCAAAGATGCAATGAGTACACTACTGGCTGAGCTCACAAACCTCTGCATATAC 480

QY 481 ATGACTCTCTCTGCTCTCAAGAGTTGGCTATTTGCTCATCCACCTGCTGCTG 540

Db 481 ATGACTCTCTCTGCTCTCAAGAGTTGGCTATTTGCTCATCCACCTGCTGCTG 540

QY 541 CTAGAAAGACGCTTCTGCTGAATGAGAATATAACAGGGTGCACAGGA 600

Db 541 CTAGAAAGACGCTTCTGCTGAATGAGAATATAACAGGGTGCACAGGA 600

QY 601 GGCATCTTCTCATGGTTGCTCTAGAAGCTCTGAGCTCTGAGATCTGAGGTC 660

Db 601 GGCATCTTCTCATGGTTGCTCTAGAAGCTCTGAGCTCTGAGATCTGAGGTC 660

QY 661 TTCTTCTGGTTGGCCATTCTGCTCATGTTGACTATCTCATATTGTA 720

Db 661 TTCTTCTGGTTGGCCATTCTGCTCATGTTGACTATCTCATATTGTA 720

QY 721 TAACGGTTTCAACCAGTGACACAGAGACCTCTCTGTAATACTAGGAAAT 780

Db 721 TAACGGTTTCAACCAGTGACACAGAGACCTCTCTGTAATACTAGGAAAT 780

QY 781 AGCCACGCGGATCTCCAGACCAATCTCTCCAGGAGACTCTCTGTAATACTAGGAAAT 780

Db 781 AGCCACGCGGATCTCCAGACCAATCTCTCCAGGAGACTCTCTGTAATACTAGGAAAT 780

QY 840 841 AAATAGCCCTGCTATGGTAGACATCTGGGCTCTAGCTTGCCCTCTCTAGTG 900

Db 840 841 AAATAGCCCTGCTATGGTAGACATCTGGGCTCTAGCTTGCCCTCTCTAGTG 900

QY 900 901 TTCTTAATCAGATACTGCTGAGCTTCTAGCTTGCCCTCTCTTAGTG 960

Db 901 TTCTTAATCAGATACTGCTGAGCTTCTAGCTTGCCCTCTCTTAGTG 960

QY 960 TTCTTAGTGAATTATGGGGTTTCCCTAAAGCAAAATAATTAAAAATG 1020

Db 960 TTCTTAGTGAATTATGGGGTTTCCCTAAAGCAAAATAATTAAAAATG 1020

QY 61 GATAAACACTTGATGAGTTCCCAAGCCACTATTTCTTCATGCT 120

Db 61 GATAAACACTTGATGAGTTCCCAAGCCACTATTTCTTCATGCT 120

RESULT 4

US-10-643-795A-23

; Sequence 23, Application US/10643795A

; Publication No. US2004041709A1

; GENERAL INFORMATION:

APPLICANT: FREDERIC J. DESAUVAGE
 APPLICANT: GRETCHEN FRANTZ
 APPLICANT: KENNETH J. HILLAN
 APPLICANT: PAUL POLAKIS
 APPLICANT: ANDREW POLSON
 APPLICANT: VICTORIA SMITH
 APPLICANT: SUSAN D. SPENCER
 APPLICANT: THOMAS D. WU
 APPLICANT: ZEMIN ZHANG

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FILE REFERENCE: P5026R1-US

CURRENT APPLICATION NUMBER: US 10/643, 795A

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: US 60/404, 809

PRIOR FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: US 60/405, 645

PRIOR FILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: US 60/413, 192

PRIOR FILING DATE: 2002-09-23

PRIOR APPLICATION NUMBER: US 60/419, 008

PRIOR FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: US 60/426, 847

PRIOR FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US 60/484, 959

PRIOR FILING DATE: 2003-07-02

NUMBER OF SEQ ID NOS: 158

SEQ ID NO: 23

LENGTH: 1395

TYPE: DNA

ORGANISM: Homo sapien

US-10-643-795A-23

Query Match 98 %; Score 1013.8; DB 8; Length 1395; Best Local Similarity 99 %; Pred. No. 1.1e-289; Matches 1015; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CAAGAGTTGGCaaaaatacgttatggccatggaaacaaacttatacgat 63
 Db 379 CAAGAGTTGGCaaaaatacgttatggccatggaaacaaacttatacgat 438

QY 64 AACAACTTGATGCGATGTTCCCCAACGCCACTATTTCCTCTCAATTGTGA 123
 Db 439 AACAACTTGATGCGATGTTCCCCAACCCACTATTTCCTCTCAATTGTGA 498

QY 124 ACAAGACTCCGAGACGGCTGGACATACCTTGTCTCTGAGAAATTCCCTGATGTT 183
 Db 499 ACAAGACTCCGAGACGGCTGGACATACCTTGTCTCTGAGAAATTCCCTGATGTT 558

QY 184 ATTAAGATACATGGCAAGAAAAGAGAGCACAGATCTGGATCCAGGGGAC 243
 Db 559 ATTAAGATACATGGCAAGAAAAGAGAGCACAGATCTGGATCCAGGGGAC 618

QY 244 ACCATGAGACTAACACACTACATGAATTACTGGTACCGTGGCAGAAAGTC 303
 Db 619 ACCATGAGACTAACACACTACATGAATTACTGGTACCGTGGCAGAAAGTC 678

QY 304 CTGGCAAAAGACACAGATGATCGTCAGACATGAAATAAACGGATGATCAA 363
 Db 679 CTGGCAAAAGACACAGATGATCGTCAGACATGAAATAAACGGATGATCAA 738

QY 364 GAAATTATCTTCTCCAAATAAGACGGATGTCATCACATGGATCCAAAGACATGT 423
 Db 739 GAAATTATCTTCTCCAAATAAGACAGATGATCATCACATGGATCCAAAGACATGT 798

QY 424 TCAAAGATGAAATGATACTACTGCTGGACTCACAAACACTCTGCAATTACATG 483
 Db 799 TCAAAGATGAAATGATACTACTGCTGGACTCACAAACACTCTGCAATTACATG 858

QY 484 TACCTCTCTCTGCTCCAACTGAGTGTGCTATTGCCATCATCACCTGCTGCT 543
 Db 859 TACCTCTCTCTGCTCCAACTGAGTGTGCTATTGCCATCATCACCTGCTGCT 918

OY 544 AGAGAAAGGCTTCTGGCAATGGAGAAGAACTACAGACGGGCGACAGGGC 603
 Db 919 AGAGAAAGGCTTCTGGCAATGGAGAAGAACTACAGACGGGCGACAGGGC 978

OY 604 CACCTTCTCATGGTTATGTCCTAGAACGGCTCTGAGGATCTAGTGGCTT 663
 Db 979 CACCTTCTCATGGTTATGTCCTAGAACGGCTCTGAGGATCTAGTGGCTT 1038

OY 664 CTTCTGAGTTGGCCATTCTAGTCATGTCATGTCATGTCATGTCATGTC 723
 Db 1039 CTTCTGAGTTGGCCATTCTAGTCATGTCATGTCATGTCATGTCATGTC 1098

OY 724 CGGTTTCTAACCGTGCAGCACAGAGAACCTCACTGTGAGTATCTATATTGATAA 783
 Db 1099 CGGTTTCTAACCGTGCAGCACAGAGAACCTCACTGTGAGTATCTATATTGATAA 1158

OY 784 CACCGGTCTCCAGCACAACTCTCCATGTTTCCAGCTCTCCAGCCACCCAA 843
 Db 1159 CACCGGTCTCCAGCACAACTCTCCATGTTTCCAGCTCTCCAGCCACCCAA 1218

OY 844 TAGGCCCTCTATAGTGAGACATCTGGGCTCTAGCCTGTCCTCCAGCCACCCAA 903
 Db 1219 TAGGCCCTCTATAGTGAGACATCTGGGCTCTAGCCTGTCCTCCAGCCACCCAA 1278

OY 904 TTAAATCAGATAACTGCTGGAGACATCTGGGCTCTAGCCTGTCCTCCAGCCACCCAA 963
 Db 1279 TTAAATCAGATAACTGCTGGAGACATCTGGGCTCTAGCCTGTCCTCCAGCCACCCAA 1338

OY 964 CTAGTGATAATGCTGGCTGTTTCCGTAATAAGCAATAATTAAAGATG 1020
 Db 1339 CTAGTGATAATGCTGGCTGTTTCCGTAATAAGCAATAATTAAAGATG 1395

RESULT 5
 US-10-948-518-23

Sequence 23, Application US/10948518

Publication No. US20050064492A1

GENERAL INFORMATION:

APPLICANT: FREDERIC J. DESAUVAGE
 APPLICANT: GRETCHEN FRANTZ
 APPLICANT: KENNETH J. HILLAN
 APPLICANT: PAUL POLAKIS
 APPLICANT: ANDREW POLSON
 APPLICANT: VICTORIA SMITH
 APPLICANT: SUSAN D. SPENCER
 APPLICANT: THOMAS D. WU
 APPLICANT: ZEMIN ZHANG

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FILE REFERENCE: P5026R1-US

CURRENT APPLICATION NUMBER: US/10/948, 518

CURRENT FILING DATE: 2004-09-22

PRIOR APPLICATION NUMBER: US 10/643, 795

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: US 60/404, 809

PRIOR FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: US 60/405, 645

PRIOR FILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: US 60/413, 192

PRIOR FILING DATE: 2002-09-23

PRIOR APPLICATION NUMBER: US 60/419, 008

PRIOR FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: US 60/426, 847

PRIOR FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US 60/484, 959

PRIOR FILING DATE: 2003-07-02

NUMBER OF SEQ ID NOS: 158

SEQ ID NO: 23

LENGTH: 1395

TYPE: DNA

ORGANISM: Homo sapien

US-10-948-518-23

Query	Match	Score	DB	Length
	Best Local Similarity	99.7%	9	1395;
	Conservative	99.8%	Pred.	No. 1..e-289;
		0;	Mismatches	2;
		0;	Matches	1015;
		0;	Indices	0;
		0;	Gaps	0
4	CAAGAGTGGCAAATACTCAAGGTTATGGTCCCGAACAAAGCTTACATTACAGT	63		
379	CAAGAGTGGCAAATACTCAAGGTTATGGTCCCGAACAAAGCTTACATTACAGT	4381		
64	AAACACTGTGGAGATGTTCCCAASGCCACTTTCCTCTTCAATGCGAA	1231		
499	ACAAAGTCCAGAAGGCTGGACATACTTGTCTTGAGAATTTCCTGAGTT	5587		
439	AAACACTGTGGAGATGTTCCCAASGCCACTTTCCTCTTCAATGCGAA	4988		
124	ACAAGCTCCAGAAGGCTGGAGACATRACTCTTGTCTTGAGAATTTCCTGAGTT	1831		
491	AAACACTGTGGAGATGTTCCCAASGCCACTTTCCTCTTCAATGCGAA	1231		
184	ATTAGATACATGGCAAGAAAGAAAGAGAACACCGTTCTGGATGCCAGGGAC	2431		
619	ACCATGAGACTAAAGCACATACATGAAATTAGCTGGTAACGGCCAGAACAA	6788		
60	559 ATTAGATACATGGCAAGAAAGAGAACACCGTTCTGGATGCCAGGGAC	6181		
244	ACCATGAGACTAAAGCACATACATGAAATTAGCTGGTAACGGCCAGAACAA	3031		
679	CTGGACAAAGAACACAGATGTTGGACAGATAATAACGGAGTGTACAA	7389		
6	619 ACCATGAGACTAAAGCACATACATGAAATTAGCTGGATGCCAGGGAC	6788		
304	CTGGACAAAGAACACAGATGTTGGACAGATAATAACGGAGTGTACAA	3631		
739	GAATAATTCTTCTCCAAATAAGAGGATGTCATGAGATAATAACGGAGTGTACAA	7988		
6	679 CTGGACAAAGAACACAGATGTTGGACAGATAATAACGGAGTGTACAA	7389		
364	GAATAATTCTTCTCCAAATAAGAGGATGTCATGAGATAATAACGGAGTGTACAA	4231		
799	739 GAATAATTCTTCTCCAAATAAGAGGATGTCATGAGATAATAACGGAGTGTACAA	7988		
424	TCAAAGAGTCAAATGTAACACTACTCTGTCAGCTGAGCTCAACACCTTGCAATTACG	4831		
60	799 TCAAAGAGTCAAATGTAACACTACTCTGTCAGCTGAGCTCAACACCTTGCAATTACG	8588		
544	TACCTCCCTGCTCCTCAAGAGTGTCTATTTCGCATCATCACCTGCTGCTCCT	5431		
919	859 TACCTCCCTGCTCCTCAAGAGTGTCTATTTCGCATCATCACCTGCTGCTCCT	9181		
604	AGAAGAACGCTTCTGTCAGCTGAGCTGAGGAAATCATACAGACGGTGGACAGGGC	6031		
979	919 AGAAGAACGCTTCTGTCAGCTGAGGAAATCATACAGACGGTGGACAGGGC	9788		
654	CATCTTCTCATCGGTTATGTCCTAGAGGCTTCTGAGGATGTAGTGGCTT	6631		
1039	604 CATCTTCTCATCGGTTATGTCCTAGAGGCTTCTGAGGATGTAGTGGCTT	6631		
724	CTTCTGTTCAACACTGGCAACIGAGAACCTCACTCTGTTATAGATGGGAAGTC	7831		
1099	724 CTTCTGTTCAACACTGGCAACIGAGAACCTCACTCTGTTATAGATGGGAAGTC	7831		
784	CGGGTTCAACACTGGCAACAGAACCTCACTCTGTTATAGATGGGAAGTC	1151		
1119	1099 CGGGTTCAACACTGGCAACAGAACCTCACTCTGTTATAGATGGGAAGTC	1151		
844	TTAATCAGATACCTGGAGCTTCATTTACAGCTCTGAGGAGCTCTTGT	9631		
1219	844 TTAAATCAGATACCTGGAGCTTCATTTACAGCTCTGAGGAGCTCTTGT	9031		
9	1219 TAGGCCCTGCTATAGTGTAGACATCTGGCCGCTCTGCTCTCTAGTGTCT	12771		
904	9 TAGGCCCTGCTATAGTGTAGACATCTGGCCGCTCTGCTCTCTAGTGTCT	13331		
9	904 TTAAATCAGATACCTGGAGCTTCATTTACAGCTCTGAGGAGCTCTTGT	9631		
1279	9 TTAAATCAGATACCTGGAGCTTCATTTACAGCTCTGAGGAGCTCTTGT	1020		
1339	1279 TTAAATCAGATACCTGGAGCTTCATTTACAGCTCTGAGGAGCTCTTGT	1395		

RESULT 6
US-10-101-510-492
; Sequence 492, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/1011,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 492
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-492

QY 739 TGGGCACACAGAGAACCTCCTCTGTAATACAACTGAGGATAGCCACGGATCTCG 798
Db 1511 TGGGCACACAGAGAACCTCCTCTGTAATACAACTGAGGATAGCCACGGATCTCG 1570
QY 799 CACCAACTCTTCACTGTTCCACAGCTCTCCAGGCCACCAATAGGCCCTCATAG 838
Db 1571 CACCAACTCTTCACTGTTCCACAGCTCTCCAGGCCACCAATAGGCCCTCATAG 630
QY 859 TGTAGACATCTGCGCGCTCTAGCTGTCCCTCTAGTGTCTTATCAGATACT 918
Db 1631 TGTAGACATCTGCGCGCTCTAGCTGTCTTATCAGATACT 1690
QY 919 GCCTCTGAASGCCCTCACTTACAACCCCTGAGCAGTCAGTGTCTTGTATTCT 978
Db 1691 GCCTCTGAASGCCCTCACTTACAACCCCTGAGCAGTCAGTGTCTTGTATTCT 1750
QY 979 GGTGTTTCTCCGTAATAAGCAAAATAATTAAAATGAAAGTT 1027
Db 1751 GGTGTTTCTCCGTAATAAGCAAAATAATTAAAATGAAAGTT 1799

RESULT 7
US-09-957-708-16
; Sequence 16, Application US/09957108
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shuijath
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific
; FILE REFERENCE: DEX 0239
; CURRENT APPLICATION NUMBER: US/09/957, 708
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 6/223, 746
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1418
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-957-708-16

Query Match 92.1%; Score 945, 6; DB 3; Length 1418;
Best Local Similarity 97.8%; Pred. No. 1.9e-269;
Matches 1001; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY 4 CRAAGAGTTGGCAAAAAATCAAGTATTGTCGGGACAAAGCTTATCAAGAT 63
Db 379 CAAGACTTGGCAAAAAATCAAGTATTGTCGGGACAAAGCTTATCAAGAT 438
QY 64 AACAACTGTGCGIAGTGTCCCAAGCCATATTTCCTCTCTCAATCTGAA 123
Db 439 AACAACTGTGCGIAGTGTCCCAAGCCATATTTCCTCTCTCAATCTGAA 498
QY 124 ACAGCTCCGAAGCTGGACATCTTGTCTCTGAGAATTTCCTGATGT 183
Db 499 ACAGCTCCGAAGCTGGACATCTTGTCTCTGAGAATTTCCTGATGT 558
QY 184 ATTAACTACATGGCAAGAAAAGAGGAGCACGATTGGATCCAGGGAAC 243
Db 559 ATTAACTACATGGCAAGAAAAGAGGAGCACGATTGGATCCAGGGAAC 618
QY 244 ACCATGAGAGCTAACCAACTACATGAAATTACCTGTTAACGGTGCAGAAGTC 303
Db 619 ACCATGAGAGCTAACCAACTACATGAAATTACCTGTTAACGGTGCAGAAGTC 678
QY 304 CTGGACAAGAGACAGATGATCGTCAGAGATGAGAATTAACGGATGTC 363
Db 679 CTGGACAAGAGACAGATGATCGTCAGAGATGAGAATTAACGGATGTC 738

RESULT 8
US-09-925-300-58
; Sequence 58, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925, 300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05968
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 6/0124, 270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1830
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; NAME/KEY: misc feature
; LOCATION: (135)

OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (432)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (443)
 OTHER INFORMATION: n equals a,t,g, or c
 US-09-925-300-58

Query Match 88.2%; Score 906; DB 3; Length 1155;
 Best Local Similarity 97.8%; Pred. No. 9_8e-258; Mismatches 8; Indels 5; Gaps 4;
 Matches 951; Conservative 8; Nucleotides 911; Sequence 317; Sequence ID: US-09-954-456-317
 Db 160 CTGATAAACACTGTGAGATCTTCCCAAGCCCCACTATTTCCTCCTCAATG 118
 Qy 59 CAGATAAACACTGTGAGATCTTCCCAAGCCCCACTATTTCCTCCTCAATG 118
 Db 219 CTGAAACAAACTCTCGAGAGGTGAGATCTTCCCAAGCCCCACTATTTCCTCCTCAATG 218
 Qy 179 ATGTTAATAGTACATGGCGAAGAAGGAGAACACAGCTCTGGGATCCAGAGG 238
 Db 279 ATTTTATAGTACATGGCGAAGAAGGAGAACACAGCTCTGGGATCCAGAGG 338
 Qy 239 GG - AACATCATGAGACTAACGACACATACGAAATTAGCTTGTTAACGG 296
 Db 339 GGGAAACACCATGGAGACTAACGACACATACGAAATTAGCTTGTTAACGG 398
 Qy 297 AACATCACTGGCGAAGAACAGATGTATCT-CAGCATGG-AATA-TAAAACCGA 354
 Db 399 AAAGTCACTGGCGAACAGAACAGATGTATCT-CAGCATGG-AATA-TAAAACCGA 458
 Db 355 GTTGATCAAGAAATTCTTCTCCAATAAAGCGGATGTCATCACATGATCCCAA 414
 Db 459 GTGATCAAGAAATTCTTCTCCAATAAAGCGGATGTCATCACATGATCCCAA 518
 Qy 415 GACATTGTCAAAGATCAATGATACACTACTGCTGCGACGTCAAAACCTCTCA 474
 Db 519 GACAATGTCAAAGATCAATGATACACTACTGCTGCGACTCACAAACCTCTCA 578
 Qy 475 TATCACATGTCACCTCTCTGTCCTCAAGATGGTGTATTTGCCATCACCTGC 534
 Db 535 TGTCTGCTTAGAGAACGGGTTCTGCTGCAATGAGAACATCAAGACGGTGGCA 594
 Qy 539 TGTCTGCTTAGAGAACGGGTTCTGCTGCAATGAGAACATCAAGACGGTGGCA 638
 Db 639 TGCTGCTTAGAGAACGGGTTCTGCTGCAATGAGAACATCAAGACGGTGGCA 698
 Qy 595 CAAGAGAGCATCTTCTCTGCTGCTGAGCTCTCTGAGATCTG 654
 Db 699 CAAGAGAGCATCTTCTCTGCTGCTGAGCTCTCTGAGATCTG 758
 Qy 655 TGGCTTCTCTGGGTTGGCCATTCTGCTCATGCTGCTATCTCATTT 714
 Db 759 TGSGCTTCTCTGGGTTGGCCATTCTGCTCATGCTGCTATCTCATTT 818
 Qy 715 ATGTTAAGGTTTCAACAGTGGGAACAGAACCTCTCTGTTACAAATG 774
 Db 819 ATGTTAAGGTTTCAACAGTGGGAACAGAACCTCTCTGTTACAAATG 878
 Qy 835 CAACCAAAATAGCGSCCTGCTATGTTAGTACATCTGGGCTCTAGCTTGGCCCTC 894
 Db 939 CAACCCAATAGCGSCCTGCTATGTTAGTACATCTGGGCTCTAGCTTGGCCCTC 998
 Qy 895 TAGTGTCTTAATGAGTACCTGGAGCTTCAACGCCCTGAGAGG 954
 Db 999 TTAGTGTCTTAATGAGTACCTGGAGCTTCAACGCCCTGAGAGG 058

RESULT 9
 US-09-954-456-317
 ; Sequence 317; Sequence ID: US-09-954-456
 ; Patent No. US20020115057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young Paul
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
 ; TITLE OF INVENTION: Sets
 ; CURRENT APPLICATION NUMBER: US/09/954,456
 ; CURRENT FILING DATE: 2001-09-18
 ; PRIORITY NUMBER: US/60/233,617
 ; PRIORITY FILING DATE: 2000-09-18
 ; PRIORITY NUMBER: US/60/234,052
 ; PRIORITY FILING DATE: 2000-09-20
 ; PRIORITY APPLICATION NUMBER: US/60/234,923
 ; PRIORITY FILING DATE: 2000-09-25
 ; PRIORITY APPLICATION NUMBER: US/60/235,134
 ; PRIORITY FILING DATE: 2000-09-25
 ; PRIORITY APPLICATION NUMBER: US/60/235,637
 ; PRIORITY FILING DATE: 2000-09-26
 ; PRIORITY APPLICATION NUMBER: US/60/235,840
 ; PRIORITY FILING DATE: 2000-09-27
 ; PRIORITY APPLICATION NUMBER: US/60/235,863
 ; PRIORITY FILING DATE: 2000-09-27
 ; PRIORITY APPLICATION NUMBER: US/60/235,720
 ; PRIORITY FILING DATE: 2000-09-27
 ; PRIORITY APPLICATION NUMBER: US/60/235,840
 ; PRIORITY FILING DATE: 2000-09-27
 ; PRIORITY APPLICATION NUMBER: US/60/235,863
 ; PRIORITY FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 317
 ; LENGTH: 1421
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-954-456-317

Query Match 87.8%; Score 902.2; DB 3; Length 1421;
 Best Local Similarity 92.8%; Pred. No. 1_5e-266; Mismatches 0; Indels 28; Gaps 1;
 Matches 977; Conservative 0; Nucleotides 911; Sequence 317; Sequence ID: US-09-954-456-317
 Db 369 ATGAAACATCTTGGCTGAGAACACTTGTGCTGAGATCTG 428
 Qy 80 ATGTTCCCGAACGCCCTATTTCTCTCAATGCTGAGAACAGCTCAGAGG 139
 Db 429 ATGTTCCCGAACGCCCTATTTCTCTCAATGCTGAGAACAGCTCAGAGG 488
 Qy 140 CTGGACATACCTTGGCTGAGAACACTTGTGCTGAGATCTG 199
 Db 489 CTGGACATACCTTGGCTGAGAACACTTGTGCTGAGATCTG 548
 Db 200 AAGAAAGAGAACGACAGATCTGGATCCAGGGAGAACCTGAGACTAAG 259
 Db 549 AAGAAAGAGAACGACAGATCTGGATCCAGGGAGAACCTGAGACTAAG 608
 Qy 250 ACACATACATGAAATTGCTGCTGAGAACGCTCAGAACAGACCA 319
 Db 609 ACACATACATGAAATTGCTGCTGAGAACGCTCAGAACAGACCA 668
 Qy 320 GATGATGTCAGACATGAGAAATAAAACGGAGTTGATCAGAAATTCTTCCTC 379

QY 752 AACCTCACTCTGTRATACATGAGGAATAGCCRCGGCATCTCCAGCACCAATTCTC 811

Db 1149 AACCTCACTCTGTAATAACATGAGGAATAGCCATGCGCTTCAGCACCAATTCTC 1208

QY 812 ATGTTTCCACAGCTCTCCAGGCCAACCAATAGCGCTGTATAGTGAGCATCC 871

Db 1209 ATGTTTCCACAGCTCTCCAGGCCAACCAATAGCGCTGTATAGTGAGCATCC 1268

QY 872 CGCTCTGAGCTGTCCTCTCTAGTGTCTTAATGAGAATCTGCCTGAGACCT 931

Db 1329 TCATTCTACGCCTGAGCAGTCTCTGTAGTGTAACTGAGCTGCCT 1388

QY 992 GTATTAAGCAAATAATTAAATAATGAAA 1024

Db 1389 GATAAAGCAAATAATTAAATAATGAAA 1421

RESULT 11

; Sequence 676, Application US/09960706

; Publication No. US20030114280A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia

; FILE REFERENCE: 4421-5029-01US

; CURRENT APPLICATION NUMBER: US/09/960,706

; CURRENT FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 60/1223,323

; PRIOR FILING DATE: 2000-08-07

; PRIOR APPLICATION NUMBER: 09/873,319

; PRIOR FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 1124

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 676

; LENGTH: 1586

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: OTHER INFORMATION: Genbank Accession No. US20030134280A1 M30894

Query Match

Best Local Similarity 88.4%; Score 838; DB 3; Length 1586;

Matches 962; Conservative 0; Mismatches 30; Indels 96; Gaps 1;

QY 20 AAATCAAGTATTGTCGGAAACAAAGCTTATCATTCAGATAAACACTGTGCG 79

Db 499 ATAAGAACACTTGTGCAAGAACACTGTGTCAGATAAACACTGTGCG 558

QY 80 ATGTTCCCCAACCCACTATTTCTCTCTCATGTAACAAAGCTCGNAGG 139

Db 559 ATGTTCCCCAACCCACTATTTCTCTCTCATGTAACAAACTCCAGAAC 618

QY 140 CTGGACACATCTTGTCTCTGAGAAATTCTCCATGATGTTAATGATACTGCG 199

Db 619 CTGGACACATCTTGTCTCTGAGAAATTCTCCATGATGTTAATGATACTGCG 678

QY 200 AAGAAAGAGAGACACAGATCTGGATCCAGGAGGAAACCCATGAGAACCTAAC 259

Db 679 AAGAAAGAGAGACACAGATCTGGATCCAGGAGGAAACCCATGAGAACCTAAC 738

QY 260 ACACATACATGAATTAGCTGGTAACGGCGGAAAGTCACTGGACAGACACA 319

Db 739 ACACATACATGAATTAGCTGGTAACGGCGGAAAGTCACTGGACAGACACA 798

RESULT 12

; Sequence 424, Application US/09873319A

; Publication No. US2003013424A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; APPLICANT: Kulkarni, Prakash

; APPLICANT: Getzenberg, Robert H.

; APPLICANT: Waga, Iwao

; APPLICANT: Yamamoto, Jun

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using Gene Expression Profiles

; FILE REFERENCE: 4421-5029-US

; CURRENT APPLICATION NUMBER: US/09/873,319A

; EARLIER APPLICATION NUMBER: US 60/1223,323

; EARLIER FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 755
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 424
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: OTHER INFORMATION: Genbank Accession No. US20030134324A1 M30894
; US-09-873-319-424
Query Match 81.6%; Score 838; DB 3; Length 1586;
Best Local Similarity 88.4%; Pred. No. 1.8e-237;
Matches 962; Conservative 0; Mismatches 30; Indels 96; Gaps 1;
QY 20 AAATCAAGGTTATTGTCGGAAACAAGTTATCATTCAGATAAACACTGTATGCAG 79
Db 499 ATAGAAACTCTTGGCAGTGACACACTGTGTGTCAGATAAACACTGTATGCAG 558
QY 80 ATGTTTCCGCCAACCCAACTTTTCTTCATATGCTGAAACAAGCTTACATGCGAGG 139
Db 559 ATGTTTCCGCCAACCCAACTTTTCTTCATATGCTGAAACAAGCTTACATGCGAGG 618
QY 140 CTGGACATACCTTGTCTTGTGAAATTTCCTGTGTTATAGATACATGCC 119
Db 619 CTGGACATACCTTGTCTTGTGAAATTTCCTGTGTTATAGATACATGCC 678
QY 200 AAGAAAGAAGAGCACACCGATCTGGGATCCAGGGGAACACATGAGACTAACG 259
Db 679 AAGAAAGAAGAGCACACCGATCTGGGATCCAGGGGAACACATGAGACTAACG 718
QY 260 ACACATACAGAAATTAGCTGGTAAACGGTCCAGAAAGTCACTGGACAAAGACA 319
Db 739 ACACATACATGAAATTAGCTGGTAAACGGTCCAGAAAGTCACTGGACAAAGACA 798
QY 320 GATGATCGAGATGAGATAATAAACGGAGTTGATCAAGAAATTATCTTCTC 379
Db 799 GATGATCGAGATGAGATAATAAACGGAGTTGATCAAGAAATTATCTTCTC 858
QY 380 CAATAAGAC------389
Db 859 CAATAAGACAGATCTCACCAAGCTGATCCAAAGACAGTATTCAAAGATGCAATG 918
QY 390 -----GGATGTCATCACA 403
Db 919 ATGTCACCAAGCTGGATCCAAATACAAATTCAAGGATGCAAATGATGTCATCACA 978
QY 404 TGGATCCAAAGACAACTTGTCAAAGATGCAAAATGATCAACTGCTGCAAGTCAAA 463
Db 979 TGGATCCAAAGACAACTTGTCAAAGATGCAAAATGATCAACTGCTGCAAGTCAAA 1038
QY 464 ACACCTCTGCTATTCATGACTCTCTCTGCTCTCAAGAGTGTGGTATTGCGCA 523
Db 1039 ACACCTCTGCTATTCATGACTCTCTCTGCTCTCAAGAGTGTGGTATTGCGCA 1098
QY 524 TCACTACCTGTGTCTGCTAGAAGAACGGTTCTGCTCAATGAGAACTACATAC 583
Db 1099 TCACTACCTGTGTCTGCTAGAAGAACGGTTCTGCTCAATGAGAACTACATAC 1158
QY 584 AGACGAGTGGCAAAAGGGCACTTCTTCATGGTTATGTCCTAGAGGTCTC 643
Db 1159 AGACGAGTGGCAAAAGGGCACTTCTTCATGGTTATGTCCTAGAGGTCTC 1218
QY 644 TGAGGACTAGTGGCTTTCGGGTTGGGCAATTCAAGTCTGTTGACT 703
Db 1219 TGAGGACTAGTGGCTTTCGGGTTGGGCAATTCAAGTCTGTTGACT 1278
QY 704 ATTCATACATGATGATAAGGGTTCAAAACAGTGGCAACAGAGAACCTCTG 763
Db 1279 ATTCATACATGATGATAAGGGTTCAAAACAGTGGCAACAGAGAACCTCTG 1338
QY 764 TAATACACATGAGGATAGCCAGCGGATCTCCAGCAACAGAGAACCTCTG 823
Db 1339 TAATACACATGAGGATAGCCATGGCGATCTCCAGCACCAATCTCCATGTTCCACA 1398

RESULT 13
US-10-847-918-14
; Sequence 14, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xionbing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 038896-126000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIORITY FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 14
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-847-918-14
Query Match 81.6%; Score 838; DB 9; Length 1586;
Best Local Similarity 88.4%; Pred. No. 1.8e-237;
Matches 962; Conservative 0; Mismatches 30; Indels 96; Gaps 1;
QY 20 AAATCAAGGTTATTGTCGGAAACAAGTTATCATTCAGATAAACACTGTATGCAG 79
Db 499 ATAGAAACTCTTGGCAGTGACACACTGTGTGTCAGATAAACACTGTATGCAG 558
QY 80 ATGTTTCCGCCAACCCAACTTTTCTTCATATGCTGAAACAAGCTTACATGCGAGG 139
Db 619 CTGGACATACCTTGTCTTGTGAAATTTCCTGTGTTATAGATACATGCC 678
QY 200 AAGAAAGAAGAGCACACCGATCTGGGATCCAGGGGAACACATGAGACTAACG 259
Db 679 AAGAAAGAAGAGCACACCGATCTGGGATCCAGGGGAACACATGAGACTAACG 718
QY 140 CTGGACATACCTTGTCTTGTGAAATTTCCTGTGTTATAGATACATGCC 199
Db 679 AAGAAAGAAGAGCACACCGATCTGGGATCCAGGGGAACACATGAGACTAACG 718
QY 260 ACACATACATGAAATTGCTGGTAACTGGGCAAGACTGCTGAAAGACACCA 319
Db 739 ACACATACATGAAATTGCTGGTAACTGGGCAAGACTGCTGAAAGACACCA 798
QY 320 GATGATCGAGACAGTGGGATCCAGGGGAACACATGAGACTAACG 379
Db 799 GATGATCGAGACAGTGGGATCCAGGGGAACACATGAGACTAACG 858
QY 380 CAATAAGAC------389
Db 859 CAATAAGACAGATGTCACCAAGCTGATCCAAAGACAGTATTCAAAGATGCAATG 918

QY 390 - -----GGATGTCATCAA 403
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 919 ATGTCAACACAGTGTGATCCAAATTACAATTCAAGGATGCAATGTCATCAA 978
 ; PRIORITY: 07-18
 ; PRIORITY NUMBER: 60/255, 281
 QY 404 TGGATCCAAAGAACATTTCAAAAGATGCAATGATACACTGCTGCAGTCACAA 463
 ; PRIORITY: 12-13
 ; PRIORITY NUMBER: 60/255, 281
 Db 979 TGGATCCAAAGAACATTTCAAAAGATGCAATGATACACTGCTGCAGTCACAA 1038
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 21517
 ; LENGTH: 1162
 QY 464 AACACTCTGCAATTACATGCAACCTCTCTGCTCTGAAGGTGGCTATTGCAA 523
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 Db 1039 AGCCTCTGCAATTACATGCAACCTCTCTGCTCTGAAGGTGGCTATTGCAA 1098
 ; US-10-357-930-21517
 QY 524 TCATCACCCAGTGCTGCTGCTGAGAAGCGCTTGCTGCAATGGAGAGAACATAC 583
 ; Query Match: 77.5%; Score: 795.8; DB: 8; Length: 1162;
 ; Best Local Similarity: 99.7%; Pred. No.: 5, 3e-225;
 ; Matches: 797; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;
 Db 1099 TCATCACCCAGTGCTGCTGCTGAGAAGCGCTTGCTGCAATGGAGAGAACATAC 1158
 ; SEQ ID NO: 21517
 ; LENGTH: 1162
 QY 584 AGGGGTGCAACAGGAGGCCATTTCCTCATGGTATTCTCCCTAGAGAGGCTTC 643
 ; 1159 AGGGGTGCAACAGGAGGCCATTTCCTCATGGTATTCTCCCTAGAGAGGCTTC 1218
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 644 TAGGATCTGAGTGGCTTCTCTGGTTGGCCATTCTGGTCTCATGGTACT 703
 ; 1219 TAGGATCTGAGTGGCTTCTCTGGTTGGCCATTCTGGTCTCATGGTACT 1278
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 704 ATTCATCATATTGTTACGGTTCAACACGTCGGCAACAGAACACTCTG 763
 ; 1279 ATTCATCATATTGTTACGGTTCAACACGTCGGCAACAGAACACTCTG 1338
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 764 TAATRACATGAGGATAACCCACCGGATCTCGACCAATTCTCATGTTCCA 823
 ; 1339 TAATRACATGAGGATAACCCACCGGATCTCGACCAATTCTCATGTTCCA 1398
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 824 CTCTCTCCAGCCAAACCAATTAGGGCTCTATAGTGTGAGCACTCTG 803
 ; 1459 TGRCCTCTCTTAGTGTCTTATCAGATACTGCTGGAGCCTTCATTACAG 1518
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 944 CCTGGAACGAGCTCTTGCTACTTGATTATGTTGGCTTTTCCGTAATAGCAA 1003
 ; 1519 CCTGGAACGAGCTCTTGCTACTTGATTATGTTGGCTTTTCCGTAATAGCAA 1578
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 1004 ATAATT 1011
 ; 1579 ATAATT 1586
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db RESULT 14
 ; Sequence 21517, Application US/10357930
 ; Publication No. US2004025086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endge, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US10/357, 930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785, 276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183, 319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189, 862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207, 454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211, 314
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 ; PRIORITY: 07-18
 ; PRIORITY NUMBER: 60/255, 281
 QY 709 ATCATATTGTTACGGTTCAACACGAGGGCACAGAACCTCACTCTGTTATA 768
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 682 ATCATATTGTTACGGTTCAACACGAGGGCACAGAACCTCACTCTGTTATA 623
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 759 ACATGAGGAAATGCCAGGGATCTCCAGCAATTCTCCATGTTCCACGCC 828
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 622 ACHATGAGGAAATGCCAGGGATCTCCAGCAATTCTCCATGTTCCACGCC 563
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 829 TCCAGCCACCCAAATAGGGCTGCTATGTGAGCTCCCGGGCTCTACCTTC 888
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 562 TCCAGCCACCCAAATAGGGCTGCTATGTGAGCTCCCGGGCTCTACCTTC 503
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 889 CCTCTCTTAGTGTCTTATCAGATACTGCTGGAGGCCTTCATTACAGCCCTG 948
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 502 CCTCTCTTAGTGTCTTATCAGATACTGCTGGAGGCCTTCATTACAGCCCTG 443
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 949 AACAGCTCTTGTGTTGGTGTGATTAGTGTGGTGTGTTTCCGTAATAGCAAATA 1008
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 442 AACAGCTCTTGTGTTGGTGTGATTAGTGTGGTGTGTTTCCGTAATAGCAAATA 383
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 QY 1009 TTAAAATGAAAGT 1027
 ; PRIORITY: 06-09
 ; PRIORITY NUMBER: 2119, 007
 Db 382 TTAAAATGAAAGT 364

RESULT 15
 US-10-357-930-24142/c
 ; Sequence 24142, Application US/10357930
 ; Publication No. US20040250086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiegel, Robert
 ; ENDER, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/833,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SEQ ID NO: 24142
 ; LENGTH: 1162
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-357-930-24142

Query Match 77.5%; Score 795.8; DB 8; Length 1162;
 Best Local Similarity 99.7%; Pred. No. 5.3e-225; Mismatches 797; Conservative 0; Gaps 0; Indels 0;

```

QY  229 TCCAGGAGGGCACCATGAGACTAACACATAGAAATTACCTGGTAACG 288
Db  1162 TCCAGGAGGGCACCATGAGACTAACACATAGAAATTACCTGGTAACG 1103
QY  289 GTGCCAGAAAGTCACTGGACAAAGACACAGATGTATCGTAGACATGAGATAAA 348
Db  1102 GTGCCAGAAAGTCACTGGACAAAGACACAGATGTATCGTAGACATGAGATAAA 1043
QY  349 AACGGAGTTGTCAGAAATTATCTTCCCAATAAGGAGGATCATACATGGAT 408
Db  1042 AACGGAGTTGTCAGAAATTATCTTCCCAATAAGGAGGATCATACATGGAT 983
QY  409 CCCAGAGAATTTGTCAGAAGATGCAATGATACACTTGCTGAGCTCAACACC 468
Db  982 CCCAGAGAATTTGTCAGAAGATGCAATGATACACTTGCTGAGCTCAACACC 923
QY  469 TCTGATATTCATGACTCTCTCTGCTCTCAAGAGTGGTCTATTGCTCATC 528
Db  922 TCTGATATTCATGACTCTCTCTGCTCTCAAGAGTGGTCTATTGCTCATC 863
QY  529 ACCTGCTGCTGCTCTAGAAGAACGGCTTCTGCTCAATGGAGAAATCATACAGGG 588
Db  862 ACTGCTGCTGCTGCTAGAAGAACGGCTTCTGCTCAATGGAGAAATCATACAGGG 803
QY  589 GTGCCAGAAAGGAGGATCTTCATGCTTATGCTCTGAGGCTCTGAGG 648
Db  802 GTGCCAGAAAGGAGGATCTTCATGCTTATGCTCTGAGGCTCTGAGG 743
QY  649 ATCTAGTGGCTTCTTCGGGATTCAGTCTCTGAGGCTCTGAGGCTCTGAGG 708
Db  742 ATCTAGTGGCTTCTTCGGGATTCAGTCTCTGAGGCTCTGAGGCTCTGAGG 683

```

QY 709 ATCATATGATACGGTTCAACAGCTGGCACAGAGAACCTCACTCTGATA 768
 Db 682 ATCATTATGTTACGGTTCAACAGCTGGCACAGAGAACCTCACTCTGATA 623
 QY 769 ACATGAGGAATGCCAGGGATCTCCAGCACAACTCTCATGTTCCACAGGCC 828
 Db 622 ACAATGAGAATGCCAGGGATCTCCAGCACAACTCTCATGTTCCACAGGCC 563
 QY 829 TCCAGGCCACCAATAGGCCCTCTATAGTGTAGACIOTCTGGGGCTCTAGCTGTC 888
 Db 562 TCCAGGCCACCAATAGGCCCTCTATAGTGTAGACIOTCTGGGGCTCTAGCTGTC 503
 QY 889 CCTCTCTTAGTGTCTTATCAGATACTGCCTGAGACGCTCTGGGGCTCTAGCTGTC 948
 Db 502 CCTCTCTTAGTGTCTTATCAGATACTGCCTGAGACGCTCTGGGGCTCTAGCTGTC 443
 QY 949 AAGGACTCTCTTGCTGTGTTGAAATTAGTGTGTTGTTTCCGTAATAGCAAAATAA 1008
 Db 442 AAGGAGTCTCTTGCTGTGTTGAAATTAGTGTGTTGTTTCCGTAATAGCAAAATAA 383
 QY 1009 TTAAAATGAAAGTT 1027
 Db 382 TTAAAATGAAAGTT 364

Search completed: December 11, 2005, 01:30:51
 Job time : 895 secs

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 20:30:37 ; Search time 230 Seconds

9737.199 Million cell updates/sec

Title: US-10-031-158B-13

Perfect score: 1027

Sequence: 1 gggcaagatgtggccaaaa.....atttaaaaaatgaaaagg 1027

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6_B_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/backfileseq.seq:*

9: /cgn2_6/ptodata/1/ina/backfileseq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	516.4	50.3	1080	9 5260223-3
2	449.2	43.7	825	2 US-09-156-964A-1B
3	444	43.2	511	3 US-09-020-956-72
4	444	43.2	511	3 US-09-020-607-72
5	444	43.2	511	3 US-09-439-313-72
6	444	43.2	511	3 US-09-352-616A-72
7	444	43.2	511	3 US-09-352-616A-72
8	444	43.2	511	3 US-09-222-142A-72
9	444	43.2	511	3 US-09-159-121-72
10	444	43.2	511	3 US-09-163-211-72
11	444	43.2	511	3 US-09-155-153-72
12	444	43.2	511	3 US-09-489-72
13	444	43.2	511	3 US-09-679-426-72
14	444	43.2	511	3 US-09-759-143-72
15	444	43.2	511	3 US-09-651-236-72
16	444	43.2	511	3 US-09-020-606-72
17	444	43.2	511	3 US-09-557-279-72
18	444	43.2	511	3 US-10-010-896-72
19	407	39.6	467	3 US-09-020-956-75
20	407	39.6	467	3 US-09-030-607-75
21	407	39.6	467	3 US-09-439-313-75
22	407	39.6	467	3 US-09-352-616A-75
23	407	39.6	467	3 US-09-232-149A-75
24	407	39.6	467	3 US-09-158B-13

RESULT 1

5260223-3

Patent No. 5260223

Patent No. 5260223

APPLICANT: BRENNER, MICHAEL B.; STROMINGER, JACK L.; SEIDMAN, JOHN G.; IP, STEPHEN H.; KRANGEL, MICHAEL S.

TITLE OF INVENTION: METHODS FOR DETECTION OF HUMAN GAMMA T CELL RECEPTOR

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US07/187,698

FILING DATE: 29-APR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 115,256

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: 16,252

FILING DATE: 19-PED-1987

APPLICATION NUMBER: 882,100

FILING DATE: 03-JUL-1986

SEQ ID NO:3;

LENGTH: 1080

ALIGNMENTS

Query Match Best Local Similarity 50.3%; Score 516.4; DB 9; Length 1080; Matches 590; Conservative 0; Mismatches 26; Indels 48; Gaps 1

QY 25 AGGTTATTTGGCCGGACAAAGCTTATCATACAGATAAACAACTGTGATGTT 84

Db 403 AACCTCTTGGAAGTCGACACACTGTTGTCAGATAAACAACTGTGCGAGTT 462

Db 403 AACCTCTTGGAAGTCGACACACTGTTGTCAGATAAACAACTGTGCGAGTT 462

QY 85 TCCCCAAGCCACTATTTCCTCANTGCTGAAACAAGCTGCCAGAGGCTGA 144

Db 463 TCCCCAAGCCACTATTTCCTCCTCGATGCTGAAACAAACTGCCAGAGGCTGA 522

QY 145 ATACATCTTGCTCTGAGAAATTTCCTGAGTTATAGATACATTCCTGAGAA 204

Db 523 ACATACCTTGCTCTGAGAAATTTCCTGAGTTATAGATACATTCCTGAGAA 582

QY 205 AGGAAGGCAACAGATCTGGATCCAGGGGGACACCATGAAGACTACGACACA 264

Db 583 AGGAGGCAACAGATCTGGATCCAGGGGGACACCATGAAGACTACGACACA 642

QY 265 TACGAAATTAGCTGCTGAGAAAGTCGACAAAGAACAGATGT 324

Db 643 TACGAAATTAGCTGCTGAGAAAGTCGACAAAGAACAGATGT 702

QY 325 ATGTCAGACATGAGAAATTAAACGGAGTGTGATGAGAAATTCTTCCTCCATA 384

NAME/KEY: CDS
 LOCATION: 1..825
 PUBLIC INFORMATION:
 DOCUMENT NUMBER: WO 94/12648
 FILING DATE: 25-NOV-1993
 PUBLICATION DATE: 09-JUN-1994

US-08-256-964A-1B

Query Match 43.7%; Score 449.2; DB 2; Length 825;
 Best Local Similarity 99.3%; Pred. No. 5.5e-129; Matches 451; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3 GCAGAGTTGGGCAAATAATCAGGTATTTCCTCCCTCCCTCCCTCCAGGTGTTGTCAGA 62

369 GCAGAGTTGGGCAAATAATCAGGTATTTCCTCCCTCCCTCCAGGTGTTGTCAGA 428

63 TAACAACATTGATGCCAGTGTTCCTCCAGGTATTTCCTCCCTCAATGCGGA 122

429 TAACAACATTGATGCCAGTGTTCCTCCAGGTATTTCCTCCCTCAATGCGGA 488

123 AACAAAGTCCAGAGGTGGACATACATTGTTGCTCTTGAGAATTTCCTGATG 182

489 AACAAAGTCCAGAGGTGGACATACATTGTTGCTCTTGAGAATTTCCTGATG 548

183 TATTAAGTACATTTGCAAGTGTTCCTCCAGGTATTTCCTCCATTTCTCCATGCGGA 242

549 TATTAAGTACATTTGCAAGTGTTCCTCCAGGTATTTCCTCCATTTCTCCATGCGGA 608

243 CACCATGAGACTAACGACATACATGAAATTAGCTGTTAACGAGAACGTC 302

609 CACCATGAGACTAACGACATACATGAAATTAGCTGTTAACGAGAACGTC 668

303 ACTGGACIAGAACACAGATGATGTCAGACATGAGATAATAAACGGAGTTGATCA 362

669 ACTGGACIAGAACACAGATGATGTCAGACATGAGATAATAAACGGAGTTGATCA 728

363 AGAAATTACCTTCCTCCATAAGACGATGTCAGACATGAGATAATAAACGGAGTTGATCA 422

729 AGAAATTACCTTCCTCCATAAGACGATGTCAGACATGAGATAATAAACGGAGTTGATCA 788

423 TTCAAACATGCAATGATGACATCTACTGCTGCGAG 455

789 TTCAAACATGCAATGATGACATCTACTGCTGCGAG 822

RESULT 2

US-08-256-964A-1B

Sequence 18 Application US/08256964A

PATENT NO. 5723109

GENERAL INFORMATION:

APPLICANT: BONNEVILLE, Marc

TITLE OF INVENTION: PRODUCTION OF SUBUNITS OF SOLUBLE T-RECEPTORS BY CO-TRANSFCTION, USES OF THE PRODUCTS THUS OBTAINED

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Young & Thompson

STREET: 745 South 23rd Street

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,964A

FILING DATE: 14-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92 14203

FILING DATE: 25-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: PATCH, Andrew J.

REGISTRATION NUMBER: Reg. No. 5723309 32,925

REFERENCE/DOCKET NUMBER: BB 94/449

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703/521-2297

TELEFAX: 703/685-0573

TELEX: 249425

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 825 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

RESULT 3

US-09-020-956-72/C

Sequence 72 Application US/09020956

PATENT NO. 6261562

GENERAL INFORMATION:

APPLICANT: XU, Jiangchun

APPLICANT: DILLIN, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 178

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEDD AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/020,956

FILING DATE: 09-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.427C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEX/FAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 72:
 LENGTH: 511 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE: Homo sapiens
 US-09-020-956-72

Query Match 43.2%; Score 444; DB 3; Length 511;

Best Local Similarity 91.3%; Pred. No. 1.7e-127; Mismatches 0; Indels 0; Gaps 0;
 Matches 462; Conservative 0; MisMatches 44; Indels 0; Gaps 0;

QY 492 CTCGCTCCCTCAAGAGTGTGTCTATTGGCCATCATCACCTGCTGCTAGAACAGAC 551
 DB 506 CNGTNCTCAAGAGGGGTGTTTNGCCATCATCACCTGCTGCTAGAACAGAC 447

QY 512 GCCTTCGCTGAATGGAGAACTAACAGACGGTGACAAGGGCATCTT 611
 DB 446 GGTTNTNGCTGCATGGAGAACATCACAGACGGGGACAAAGGGCATCTT 387

QY 612 CTCATCGGTTATGTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 671
 DB 386 CTCTATCGTTATGTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 327

QY 672 GTTGGGCCATTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 731
 DB 326 GTTGGGCCATTGTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 267

QY 732 AAACCAGTGGGACACAGAACCTCTACTCTGTTACAACTGAGGAATAGGCT 791
 DB 266 AAACCAGTGGGACACAGAACCTCTACTCTGTTACAACTGAGGAATAGGCT 207

QY 792 TCTCAGGACCAATCTCCATGTTCCACGCTCTCCAGCAACCCAATAGGCT 851
 DB 205 TCTCAGGACCAATCTCCATGTTCCACGCTCTCCAGCAACCCAATAGGCT 147

QY 852 GCTATAGTGTAGACATCTGGGCTCTAGCTCTGCTCTCTAGTTTAATCA 911
 DB 146 GNTATAGTGTAGACATCTGGGCTCTAGCTCTGCTCTCTAGTTTAATCA 87

QY 912 GATACTGCCTGAGACGCTTCACTTACACGCCCTGAGACAGCTCTTCTAGTGA 971
 DB 86 GATACTGCCTGAGACGCTTCACTTACACGCCCTGAGACAGCTCTTCTAGTGA 27

QY 972 ATTATGTTGGTGTGTTTCGTTA 997
 DB 26 ATTATGTTGGTGTGTTTCGTTA 1

RESULT 4
 US-09-030-607-72/C

; Sequence 72, Application us/09030607
 ; Pat. No. 626245
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US09/030,607
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-9000
 TELEX/FAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 72:
 LENGTH: 511 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE: Homo sapiens
 US-09-030-607-72

Query Match 43.2%; Score 444; DB 3; Length 511;

Best Local Similarity 91.3%; Pred. No. 1.7e-127; Mismatches 0; Indels 0; Gaps 0;
 Matches 462; Conservative 0; MisMatches 44; Indels 0; Gaps 0;

QY 492 CTCGCTCCCTCAAGAGTGTGTCTATTGGCCATCATCACCTGCTGCTAGAACAGAC 551
 DB 506 CNGTNCTCAAGAGGGGTGTTTNGCCATCATCACCTGCTGCTAGAACAGAC 447

QY 512 GCCTTCGCTGAATGGAGAACTAACAGACGGGGACAAAGGGCATCTT 611
 DB 446 GGTTNTNGCTGCATGGAGAACATCACAGACGGGGACAAAGGGCATCTT 387

QY 612 CTCATCGGTTATGTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 671
 DB 386 CTCTATCGTTATGTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 327

QY 672 GTTGGGCCATTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 731
 DB 326 GTTGGGCCATTGTCAGTCTCTGTTACTATCTCATATTGATAACGGTTTC 267

QY 732 AAACCAGTGGGACACAGAACCTCTACTCTGTTACAACTGAGGAATAGGCT 791
 DB 266 AAACCAGTGGGACACAGAACCTCTACTCTGTTACAACTGAGGAATAGGCT 207

QY 792 TCTCAGGACCAATCTCCATGTTCCACGCTCTCCAGCAACCCAATAGGCT 851
 DB 205 TCTCAGGACCAATCTCCATGTTCCACGCTCTCCAGCAACCCAATAGGCT 147

QY 852 GCTATAGTGTAGACATCTGGGCTCTAGCTCTGCTCTCTAGTTTAATCA 911
 DB 146 GNTATAGTGTAGACATCTGGGCTCTAGCTCTGCTCTCTAGTTTAATCA 87

QY 912 GATACTGCCTGAGACGCTTCACTTACACGCCCTGAGACAGCTCTTCTAGTGA 971
 DB 86 GATACTGCCTGAGACGCTTCACTTACACGCCCTGAGACAGCTCTTCTAGTGA 27

QY 972 ATTATGTTGGTGTGTTTCGTTA 997
 DB 26 ATTATGTTGGTGTGTTTCGTTA 1

RESULT 5
 US-09-139-313-72/C

; Sequence 72, Application us/09439313
 ; Pat. No. 632505
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun

RESULT 6
US-09-352-616A-72/c
; Sequence 72, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:

FILE REFERENCE: 210121-427C5
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 72
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: n = A,T,C or G
; US-09-232-149A-72
; Query Match 43.2%; Score 444; DB 3; Length 511;
; Best Local Similarity 91.3%; Pred. No. 1-7e-127;
; Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
; OTHER INFORMATION: n = A,T,C or G
; US-09-159-812-72
; Query Match 43.2%; Score 444; DB 3; Length 511;
; Best Local Similarity 91.3%; Pred. No. 1-7e-127;
; Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
; OTHER INFORMATION: n = A,T,C or G
; Qy 492 CCTGCTCCCTCAAGAGTGTGTCATTGGCCATCATCACCTGTCTGCTAGAACAC 551
; Db 506 CNGGNTCTCAAGGGGGTGTATTGGCCATCATCACCTGTCTGCTAGAACAC 447
; Qy 552 GGCTTCTGCTGAATGGAGAAATCATAACAGACGGTGGCAAGAGGCATCTT 611
; Db 446 GGTNTNTNGCTGGAATGAGAACATACAAGACGGTGGCAAGAGGCATCTT 387
; Qy 552 CCTCATCGTTATGTCCTAGAGGTTCTAGGGTCTAGAGGATCTAGTGCTGG 671
; Db 386 CTTCATCGTTATGTCCTAGAGGTTCTAGGGTCTAGAGGATCTAGTGCTGG 327
; Qy 672 GTRGGGCATTCTAGTCTCACTGTGACTATCTCATATGTCATATGTTAACGGTT 731
; Db 326 GTRGGGCATTCTAGTCTCACTGTGACTATCTCATATGTCATATGTTAACGGTT 267
; Qy 732 AACCACTGGCACACAGAGAACCTCTGTAATACATGAGGATAGGCCACGGCA 671
; Db 366 AACCACTGGCACACAGAGAACCTCTGTAATACATGAGGATAGGCCACGGCA 327
; Qy 792 TCTCAGGACCAACTCTCATGTTTCCAGGAACTCACTCTGATAACAATGGAAATAGCCACGGTT 731
; Db 206 TNTCCAGGACCAACTCTCATGTTTCCAGGAACTCACTCTGATAACAATGGAAATAGCCACGGTT 267
; Qy 852 GCTATGTTGAGACATCCCTCGGGCTTCTAGCTTCTCTGTTAGTGTCTTAATCA 911
; Db 146 GNTATAGTGTAGACATCCCTCGGGCTTCTAGCTTCTCTGTTAGTGTCTTAATCA 87
; Qy 912 GAAACTGCTGGAGCCCTTCATTTACACGCCCTGAGCAGTCTCTTGCTAGTGA 911
; Db 86 GAAACTGCTGGAGCCCTTCATTTACACGCCCTGAGCAGTCTCTTGCTAGTGA 87
; Qy 972 ATTAGTGTGTTCTCGTAA 997
; Db 26 ATATGTTGGTGTTCGTTATA 1
; RESULT 8
; US-09-159-812-72/c
; Sequence 72, Application US/09159812A
; Patent No. 6620522
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlicker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaloo, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Reitter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Veevick, Thomas S.
; APPLICANT: Carter, Darwick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skoky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-428C5
; CURRENT APPLICATION NUMBER: US/09/159, 812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 72
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: n = A,T,C or G
; US-09-159-812-72
; Query Match 43.2%; Score 444; DB 3; Length 511;
; Best Local Similarity 91.3%; Pred. No. 1-7e-127;
; Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
; OTHER INFORMATION: n = A,T,C or G
; US-09-636-215-72/c
; Sequence 72, Application US/09636215
; Patent No. 6620522
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlicker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaloo, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Reitter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Veevick, Thomas S.
; APPLICANT: Carter, Darwick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skoky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121-42717C17

CURRENT APPLICATION NUMBER: US/09/636,215
 CURRENT FILING DATE: 2000-08-10
 NUMBER OF SEQ ID NOS: 852
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 72
 LENGTH: 511
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(511)
 OTHER INFORMATION: n = A,T,C or G
 US-09-636-515-72

Query Match 43.2%; Score 444; DB 3; Length 511;
 Best Local Similarity 91.3%; Pred. No. 1..e-127;
 Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 Qy 492 CCTGTCCTCAAGAAGGGTGTCTATTGCCATCATCACCTGCGTCTGCTTAGAGAAC 551
 Db 506 CNGTNCTCAAGAGGGGTGTTTGCCATCATCACCTGCGTCTGCTTAGAGAAC 447

Qy 552 GGCTTCTCTGCGATGGAGAATACAGAGGGCGAAGAGGGCCTCTTT 611
 Db 446 GGTINNTGCTGCGATGGAGAATACAGAGGGCGAAGAGGGCCTCTTT 387

Qy 612 CCTCATCGGTATTGCTCTAGAAGGGTGTCTGCG 671
 Db 386 CTTCATCGGTATTGCTCTAGAAGGGTGTCTGCG 327

Qy 672 GTTGGCCATTCTCGATGTCATGTTGTTACTATCTATGATAACGGTTTC 731
 Db 326 GTTGGCCATTCTCGATGTCATGTTGTTACTATCTATGATAACGGTTTC 267

Qy 732 AAACAGTGGCACACAGAGAACCTACTCTGTTAACTATGAGGAATAGCCAGGGGA 791
 Db 266 AACCAAGTGGCACACAGAGAACCTACTCTGTTAACTATGAGGAATAGCCAGGGGA 207

Qy 792 TCTCCAGCACAATCTCCATGTTCCACAGGCAACCCAATAGGGCT 851
 Db 206 TNTCCAGCACAATCTCCATGTTCCACAGGCAACCCAATAGGGCT 147

Qy 852 GCTATAGCTGAGCATCTCGCGGCTCTGCGCTGCTCTCTAGTGTCTTAATCA 911
 Db 146 GNTATAGCTGAGCATCTCGCGGCTCTGCGCTGCTCTCTAGTGTCTTAATCA 87

Qy 912 GATACTGCTGGAGGCCTTCATTACAGGCCGTAAGCAGTCTTGCTGTGA 971
 Db 86 GATACTGCTGGAGGCCTTCATTACAGGCCGTAAGCAGTCTTGCTGTGA 27

Qy 972 ATTATGCTGCTGTTCCGTAATA 997
 Db 26 ATTATGCTGCTGTTCCGTAATA 1

RESULT 10
 US-09-685-166A-72/c
 Sequence 72, Application US/09685166A
 Patent No. 6630305
 GENERAL INFORMATION:
 APPLICANT: XU, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqui
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick

RESULT 11
 US-09-115-453-72/c
 Sequence 72, Application US/09115453B
 Patent No. 6657056
 GENERAL INFORMATION:
 APPLICANT: XU, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqui
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedwick, Thomas S.
 APPLICANT: Carter, Darrick

CURRENT APPLICATION NUMBER: US/09/685,166A
 CURRENT FILING DATE: 2000-10-10
 NUMBER OF SEQ ID NOS: 898
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 72
 LENGTH: 511
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(511)
 OTHER INFORMATION: n = A,T,C or G
 US-09-685-166A-72

Query Match 43.2%; Score 444; DB 3; Length 511;
 Best Local Similarity 91.3%; Pred. No. 1..e-127;
 Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 Qy 492 OCTGTCCTCAAGAGGTGTCTATTGCCATCATCACCTGCGTCTGCTTAGAGAAC 551
 Db 506 CNGTNCTCAAGAGGGGTGTTTGCCATCATCACCTGCGTCTGCTTAGAGAAC 447

Qy 552 GCCTTCTGCGCAATGGAGAATACAGACGGCCTCTTT 611
 Db 386 CTTCATCGGTATTGCTCTAGAAGGGTGTCTGCG 327

Qy 612 OCTCATCGGTATTGCTCTAGAAGGGTGTCTGCG 671
 Db 446 GGTINNTGCTGCGATGGAGAATACAGACGGCCTCTTT 387

Qy 672 GTTGGCCATTCTCGATGTCATGTTGTTACTATCTATGATAACGGTTTC 731
 Db 326 GTTGGCCATTCTCGATGTCATGTTGTTACTATCTATGATAACGGTTTC 267

Qy 732 AACCAAGTGGCACACAGAGAACCTACTCTGTTAACTATGAGGAATAGCCAGGGGA 791
 Db 386 AACCAAGTGGCACACAGAGAACCTACTCTGTTAACTATGAGGAATAGCCAGGGGA 207

Qy 792 TCTCCAGCACAATCTCCATGTTCCACAGGCAACCCAATAGGGCT 851
 Db 206 TNTCCAGCACAATCTCCATGTTCCACAGGCAACCCAATAGGGCT 147

Qy 852 GCTATAGCTGAGCATCTCGCGGCTCTGCGCTGCTCTCTAGTGTCTTAATCA 911
 Db 146 GNTATAGCTGAGCATCTCGCGGCTCTGCGCTGCTCTCTAGTGTCTTAATCA 87

Qy 912 GATACTGCTGGAGGCCTTCATTACAGGCCGTAAGCAGTCTTGCTGTGA 971
 Db 86 GATACTGCTGGAGGCCTTCATTACAGGCCGTAAGCAGTCTTGCTGTGA 27

Qy 972 ATTATGCTGCTGTTCCGTAATA 997
 Db 26 ATTATGCTGCTGTTCCGTAATA 1

CURRENT APPLICATION NUMBER: US/09/115,453B

```

; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 72
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: n = A,T,C or G
; US-09-688-489-7-2

Query Match 43.2%; Score 444; DB 3; Length 511;
Best Local Similarity 91.3%; Pred. No. 1..127; Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 492 CCTGCTCCCAAGAGGGTGCATATTGGCCATCATCACCTGCTGCTAGAAGAAC 551
Db 506 CNGTNCTCAAGAGGGGTGATTATTGGCCATCATCACCTGCTGCTAGAAGAAC 447
QY 552 GCCTTCCTGCTGCAATGGAGGAATCATAACAGACGGTGGACAAGGGGCATTT 611
Db 552 GCCTTCCTGCTGCAATGGAGGAATCATAACAGACGGTGGACAAGGGGCATTT 611
QY 446 GTTNTNTGCTGCAATGGAGGAATCATAACAGACGGGCAAGGGGCATCTT 387
Db 446 GTTNTNTGCTGCAATGGAGGAATCATAACAGACGGGCAAGGGGCATCTT 387
QY 612 CTCTACATCGGTATGTCCTAGAACGCTTCTGAGGATCTAGTGCGCTTCTTCGG 671
Db 506 CNGTNCTCAAGAGGGGTGATTATTGGCCATCATCACCTGCTGCTAGAAGAAC 447
QY 386 CTCTACATCGGTATGTCCTAGAACGCTTCTGAGGATCTAGTGCGCTTCTTCGG 327
Db 386 CTCTACATCGGTATGTCCTAGAACGCTTCTGAGGATCTAGTGCGCTTCTTCGG 327
QY 672 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 731
Db 326 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 267
QY 732 AAACCACTGGCACAGAGAACTCACTCTGTAATACATAGGAAATAGCCACGCGA 791
Db 326 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 267
QY 672 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 731
Db 266 AAACCACTGGCACAGAGAACTCACTCTGTAATACATAGGAAATAGCCACGCGA 207
QY 792 TCTCCAGGCCAACTCTCCATGTTCCACAGCTCTCCAGGAAACCCAAATAGCGCT 851
Db 206 TNTCCAGGCCAACTCTCCATGTTCCACAGCTCTCCAGGAAACCCAAATAGCGCT 147
QY 852 GCTATAGTAGTGTAGACATCCGGGCTTCTAGCCCTGCTCTCTGTTTAATCA 911
Db 145 GNTATAGTAGTGTAGACATCCGGGCTTCTAGCCCTGCTCTCTGTTTAATCA 87
QY 912 GATAACTGCCTGAAGCCCTTCAATTACGGCTGAAGGAGCTCTCTGCTAGTGA 971
Db 86 GATAACTGCCTGAAGCCCTTCAATTACGGCTGAAGGAGCTCTCTGCTAGTGA 971
QY 972 ATTATGCGTGTCTTCCGTATA 997
Db 26 ATTATGCGTGTCTTCCGTATA 1

RESULT 12
US-09-688-489-7/c
; Sequence 72, Application US/09688489
; Patent No. 679515
; GENERAL INFORMATION
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocher, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ranger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Dav, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Repler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 72
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien

; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: n = A,T,C or G
; US-09-688-489-7-2

Query Match 43.2%; Score 444; DB 3; Length 511;
Best Local Similarity 91.3%; Pred. No. 1..127; Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 492 CCTGCTCCCAAGAGGGTGCATATTGGCCATCATCACCTGCTGCTAGAAGAAC 551
Db 506 CNGTNCTCAAGAGGGGTGATTATTGGCCATCATCACCTGCTGCTAGAAGAAC 447
QY 552 GCCTTCCTGCTGCAATGGAGGAATCATAACAGACGGTGGACAAGGGGCATTT 611
Db 552 GCCTTCCTGCTGCAATGGAGGAATCATAACAGACGGTGGACAAGGGGCATTT 611
QY 446 GTTNTNTGCTGCAATGGAGGAATCATAACAGACGGGCAAGGGGCATCTT 387
Db 446 GTTNTNTGCTGCAATGGAGGAATCATAACAGACGGGCAAGGGGCATCTT 387
QY 612 CTCTACATCGGTATGTCCTAGAACGCTTCTGAGGATCTAGTGCGCTTCTTCGG 671
Db 506 CNGTNCTCAAGAGGGGTGATTATTGGCCATCATCACCTGCTGCTAGAAGAAC 447
QY 386 CTCTACATCGGTATGTCCTAGAACGCTTCTGAGGATCTAGTGCGCTTCTTCGG 327
Db 386 CTCTACATCGGTATGTCCTAGAACGCTTCTGAGGATCTAGTGCGCTTCTTCGG 327
QY 672 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 731
Db 326 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 267
QY 732 AAACCACTGGCACAGAGAACTCACTCTGTAATACATAGGAAATAGCCACGCGA 791
Db 326 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 267
QY 672 GTTGGGCATTCTAGTCTCATGTGTACTATCTATCATATTGATAACGGTTTC 731
Db 266 AAACCACTGGCACAGAGAACTCACTCTGTAATACATAGGAAATAGCCACGCGA 207
QY 792 TCTCCAGGCCAACTCTCCATGTTCCACAGCTCTCCAGGAAACCCAAATAGCGCT 851
Db 206 TNTCCAGGCCAACTCTCCATGTTCCACAGCTCTCCAGGAAACCCAAATAGCGCT 147
QY 852 GCTATAGTAGTGTAGACATCCGGGCTTCTAGCCCTGCTCTCTGTTTAATCA 911
Db 145 GNTATAGTAGTGTAGACATCCGGGCTTCTAGCCCTGCTCTCTGTTTAATCA 87
QY 912 GATAACTGCCTGAAGCCCTTCAATTACGGCTGAAGGAGCTCTCTGCTAGTGA 971
Db 86 GATAACTGCCTGAAGCCCTTCAATTACGGCTGAAGGAGCTCTCTGCTAGTGA 971
QY 972 ATTATGCGTGTCTTCCGTATA 997
Db 26 ATTATGCGTGTCTTCCGTATA 1

RESULT 13
US-09-679-426-7/c
; Sequence 72, Application US/09679426
; Patent No. 679515
; GENERAL INFORMATION
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocher, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ranger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Dav, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Repler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C0
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 72
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien

```

CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 72
LENGTH: 511
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(511)
OTHER INFORMATION: n = A,T,C or G
US-09-679-426-72

Query Match 43.2%; Score 444; DB 3; Length 511;
Best Local Similarity 91.3%; Pred. No. 1_7e-127;
Matches 462; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Db 506 CNGTNCCTCAAGAGGGGTATTGCCCCATACCTGGTTGCTTAGAACG 447
Qy 492 CCTGCTCTCAAGAGTGTTGCTATTGCCCCATACCTGGTTGCTTAGAAC 551
Db 446 GGTNTTNGCTCAATGGAGAACTAACAAGCAGGGCAACAGGCGCATCTT 387
Qy 612 CCTCATCGTTATGCTGAGAGAACTATAACGAGAGCTGAGAGCTGTTG 671
Db 552 GCCTTCGCTGCAATGGAGAGAACTATAACGAGAGCTGAGAGCTGTT 611
Db 386 CTTCATCGTTATGCTGAGAGAACTATAACGAGAGCTGAGAGCTGTT 327
Qy 672 GTTGTGSGCAATTGCTGTTGACTATCTATCTATGTTATAACGGTTTC 731
Db 326 GTTGTGSGCAATTGCTGTTGACTATCTATCTATGTTATAACGGTTTC 267
Qy 732 AAACCTGTGGCACAGAGAACTCTGTAATACAACTGAGAACTGACCGA 791
Db 266 AAACCTGTGGCACAGAGAACTCTGTAATACAACTGAGAACTGACCGA 207
Qy 792 TCTCCAGGACCAATTCTTCAGCTTTCACAGCTTCCAGCAACCAAATAGCGCT 851
Db 206 TCTCCAGGACCAATTCTTCAGCTTTCACAGCTTCCAGCAACCAAATAGCGCT 147
Qy 852 GCTATAGTGTGACATCTGCAGCTTTCACAGCTTCCAGCAACCAAATAGCGCT 911
Db 146 GNTATAGTGTGACATCTGCAGCTTTCACAGCTTCCAGCAACCAAATAGCGCT 87
Qy 912 GATRACTCCTGGAGCCTTCATTTACACGCCCTGAGAGCTCTTCTGTTG 971
Db 86 GATAACTCGCTGAACTTCATTTACACGCCCTGAGAGCTCTTCTGTTG 27
Qy 972 ATTATGTTGTTGTTCCGTTA 997
Db 26 ATTATGTTGTTGTTCCGTTA 1

RESULT 14
US-09-759-143-72/C
Sequence 72, Application US/09759143
Patient NO: 6800746
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel

RESULT 15
US-09-651-236-72/C
Sequence 72, Application US/09651236
Patient NO: 6818751
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.

```

; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vadwick, Thomas S.
; APPLICANT: Carter, Darren
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Ajun
; APPLICANT: Sheiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 72
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n = A,T,C or G
; US-09-651-236-72

Query Match 43.2%; Score 444; DB 3; Length 511;
Best Local Similarity 91.3%; Pred. No. 1..7e-127;
Matches 462; Conservancy 0; Mismatches 44; Indels 0; Gaps 0;
Matches 462; Conservatory 0; Mismatches 44; Indels 0; Gaps 0;
Qy 492 CTCGCTCCCTCAAGACTGTGCTATTTGCCATCATCACCTGGCTGTCCTAGAACAC 551
Db 506 CNGSTNCTTCAGAGGGGTGATATTNGCCATCATCACCTGGCTGTCCTAGAACAC 447
Qy 552 GCCTTTCGCTGCATGGAGAAATCATAACAGACGGCGAACAGAGGGCATCTTT 611
Db 446 GGTWNTNGCTGCATGGAGAACATCATACAGACGGGGCACAGAGGGCATCTTT 387
Qy 612 CTCTATCGTTATGTCCTAGTCCTAGAAGCTCTTGAGGATCTAGTGGCTTCTTCGG 671
Db 385 CTCTATCGTTATGTCCTAGTCCTAGAAGCTCTTGAGGATCTAGTGGCTTCTTCGG 327
Qy 672 GTTGGGCCATTCTGTTCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 731
Db 326 GTTGGCCATTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 267
Qy 732 AAACCAAGTGGCACACAGAACCTTCACTCTGTTAATACAAATAGGAATAGCCACGGGA 791
Db 266 AACCCAGTGGCACACAGAACCTTCACTCTGTTAATACAAATAGGAATAGCCACGGGA 207
Qy 792 TCTCCAGACCAATCTCCATGTTTCCACAGCTCTCCAGCCACCCAAATAGGGCT 851
Db 205 TTTCCAGACCAATCTCCATGTTTCCACAGCTCTCCAGCCACCCAAATAGGGCT 147
Qy 852 GCTATAGTGTAGACATCCTGGGCTCTAGCTGTCCTAGCTTCTTAATCA 911
Db 146 GNTATAGTGTAGACATCCTGGGCTTACGCTGTCCTGCTCTTAGTCTTAAATCA 87
Qy 912 GATACTGCCTGGAGCCCTCATTTACGGCCCTGAGCAGCTCTGCTAGTGA 971
Db 86 GATAACTGCCTGGAGCCCTCATTTACGGCCCTGAGCAGCTCTGCTAGTGA 27
Qy 972 ATTAGTGGTGTGTTTCGTAATA 977
Db 26 ATTATGTGGTGTGTTTCGTAATA 1

```

Search completed: December 10, 2005, 23:27:03
Job time : 232 secs

THIS PAGE BLANK (USPTO)

QY	637 CGTCTCTGAGGATCAGTGGCTCTTCCTGGTTGGCCATTACAGTCATGT	696
Db	541 GGTACTATTCATCATTTGTTAACGGTTCAACACCAGGGCACAGAGACT	756
Db	541 GGTACTATTCATCATTTGTTAACGGTTCAACACCAGGGCACAGAGACT	600
QY	757 CACTCTTAATACATGAGGAATACCGACATCTCCCTTGTT	816
Db	601 CACTCTTAATACATGAGGAATACCGACATCTCCCTTGTT	660
QY	817 TTCCACAGCTCTCCGCCAACCAAATAGGCCCTGTTAGTGACATCTGGGCT	876
Db	661 TTCCACAGCTCTCCGCCAACCAAATAGGCCCTGTTAGTGACATCTGGGCT	720
QY	877 TCTAGCTTGCCCTCTCTAGTGTCTTAACTGAACTAGCCCTGTTAGTGACATCTCCAGTT	936
Db	721 TCTAGCTTGCCCTCTCTAGTGTCTTAACTGAACTAGCCCTGTTAGTGACATCTCCAGTT	780
QY	937 TTACACCCCTGAGAGCTCTTGTCTAGTGAATATGTTGTGTTTCGCTAA	995
Db	781 TTACACCCCTGAGAGCTCTTGTCTAGTGAATATGTTGTGTTTCGCTAA	840
QY	996 TAGCATAATAATTAAATGAAA	1024
Db	841 TAGCATAATAATTAAATGAAA	869
RESULT 4		
BR679123	BF679123	821 bp mRNA linear EST 21-DEC-2000
DEFINITION	6021533901 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294247 5', mRNA sequence.	
ACCESSION	BF679123	
VERSION	BF679123.1	GT:11953018
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Buarchoptoglires; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	1. (bases 1 to 821) NIH_MGC http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rcs@nihmail.nih.gov	
FEATURES	Location/Qualifiers source 1. .821 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4294247" /lab_host="DHL08 (T1 phage-resistant)" /clone_id="NIH_MGC_83" /note="Organelle: prostate; Vector: pDMR-LIB (Clontech); Site 1: SFI (ggccgcgtcgcc); Site 2: SFI (ggccgtatggcc), 5', and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGCC-3'; and 3' adaptor sequence: 5'-ATCTAGAGGCCAGGCCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4	
ORIGIN		
QY	72 TGTGCGATGTTCCCCAACCCACTATTTCTCTTAACTGCTGAAACAAGCT	131
Db	62 TGTGCGATGTTCCCCAACCCACTATTTCTCTTAACTGCTGAAACAAGCT	121
QY	132 CCAGAAGGCTGAAACATACCTTGTGTCTCTGAGAAATTTCCTGATGTTATTAGAT	191
Db	122 CCAGAAGGCTGAAACATACCTTGTGTCTCTGAGAAATTTCCTGATGTTATTAGAT	181
QY	192 ACATGCGAAGAAGAAGACGACAGATCTTGTGATTCAGAGAGGGACACCATGAA	251
Db	182 ACATGCGAAGAAGAAGACGACAGATCTTGTGATTCAGAGAGGGACACCATGAA	241
QY	252 GACTAAGACACATAGTAAATTAGCTGGTTAACGGTGCAGAAAGTCCTGGACAA	311
Db	242 GACTAAGACACATAGTAAATTAGCTGGTTAACGGTGCAGAAAGTCCTGGACAA	301
QY	312 AGAACACAGATGTTCTCAGCATGAGAATTAAACGGAGITGATCAGAAATTAT	371
Db	302 AGAACACAGATGTTCTCAGCATGAGAATTAAACGGAGITGATCAGAAATTAT	361
QY	372 CTTCCTCCAAATAAGCAGGTCTCATCACATGGATCCAAAGAACATGTCAGAA	431
Db	362 CTTCCTCCAAATAAGCAGGTCTCATCACATGGATCCAAAGAACATGTCAGAA	421
QY	432 TCCAATGATACTACTGCTCAGCACACCTCTGCAATTACATCTACCTCT	491
Db	422 TCCAATGATACTACTGCTCAGCACACCTCTGCAATTACATCTACCTCT	481
QY	492 CCTGCTCTCAAGAGTGTGTTATTTGCCATCATCACCTGCTGTGTGTCTAGTCAGAA	551
Db	482 CCTGCTCTCAAGAGTGTGTTATTTGCCATCATCACCTGCTGTGTGTCTAGTCAGAA	541
QY	552 GCTTCTTGCTGCAATGAGA--GAATCATPACAGCAGGCGCAAA-GGGGCCATCT	608
Db	542 GCTTCTTGCTGCAATGAGA--GAATCATPACAGCAGGCGCAAA-GGGGCCATCT	601
QY	609 TTTCCTCATCGTTATGTCCTAG - AACGCTCTGAGATCTAGTGGCT-TCT	665
Db	602 TTTCCTCATCGTTATGTCCTAGTGGCTCTGAGATCTAGTGGCTATCT	661
QY	666 TCTGCTGTTGGCCATTCAGTCATGTTGTTACTATCTCATGTTGTTAAC	724
Db	662 TACTGGCTTAGGCCAATTCAGTCCTCATGTTGTTACTATCTCATGTTAAC	721
QY	725 GCTTTCAACACAGTGGCACAGAACCTACTGTAAATAC	770
Db	722 GG--TTACACCATGGCACAGAACCTACTGTAAATAC	765
RESULT 5		
BR678971	BF678971	997 bp mRNA linear EST 21-DEC-2000
LOCUS	6021536051 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294873 5', mRNA sequence.	
DEFINITION	BF678971	
ACCESSION	BF678971.1	GT:11952866
VERSION		
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

ORIGIN

Subtraction by Bento Soares and M. Fatima Bonaldo. "

Query Match 60.2%; Score 618 6; DB 1; Length 636;

Best Local Similarity 99.2%; Pred. No. 5.7e-15; Mismatches 4;

Matches 632; Conservative 0; Gaps 1; Gaps 1;

391 GATGTCATCACAAATGGTCCAAAGAACATTTGTCAAAGATCAAATGATACTACG 450

cDNA library arrayed by: The I.M.A.G.E. Consortium (L1NL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/L1NL at:

http://image.lnl.gov

Plate: L1CM1091 row: e column: 04

High quality sequence stop: 629.

FEATURES SOURCE High quality sequence stop: 629.

1. .902 /organism="Homo sapiens"

/mol_type="mRNA" /db_xref="taxon:9606" /clone_host="IMage:4274283" /clone_libr="NIH_MGC_83"

note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccggccgg); Site 2: SfiI (ggccatccatggcc); 5', and 3' adaptors were used in cloning and 5', adaptor sequence: 5'-CACGCCATTATGCC-3'

and 3', adaptor sequence: 5'-ATTCTAGAGGCCGAGGGCTATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

391 TAGAAGCGCTCTGTGGAGCTAGTGGCTCTCTGGTTGGCCATTGCACTC 338

391 TCACTGTTGTTACTATCTATATTGTATAACGTTTCAACAGTGGCACACAGA 750

7

BF671593

LOCUS

DEFINITION

mRNA Sequence.

ACCESSION

BF674593

VERSION

BF674593.1

KEYWORDS

EST.

SOURCE

Organism

Homo sapiens (human)

Homolog

Blastn

Blastp

Blastx

Blastn

Blastp

COMMENT

Tissue procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

Db	600	TTCCTCATGGTATAGCTGAGAGCTCTGAGAGATCCATTAGGTCTTCCTT	659
Qy	668	CTGGGT-TGGGCATTCTAGTCTCATGTG-TGACTATCTCATATTGTTAACG	725
Db	660	CTGGCTCTGGGCAATTCCAGTCATGTCATGTCATCATTATGGATAC	719
Db	726	GTTTCAACCAAGCTGGCAC	745
Qy	720	GGTTAAACCACAGGCCAC	739
RESULT 8			
LOCUS	A1685999_c	A1685999	638 bp mRNA linear EST 27-MAY-1999
DEFINITION	tg1a04_x1	NCI CGAP Pr28	Homo sapiens cDNA clone IMAGE:2248878 3'
AUTHORS			similar to gb:MI3231 T-CELL RECEPTOR GAMMA CHAIN C REGION (HUMAN);
TITLE			mRNA sequence.
ACCESSION	A1685999		
KEYWORDS			
VERSION			
SOURCE			
ORGANISM	Homo sapiens (human)		
COMMENT			
1	(bases 1 to 638)		
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Euarchoptoglires; Primates; Catarrhini; Homidae; Homo.			
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.			
CDNA Library Preparation: M. Bento Soares, Ph.D.			
CDNA Library Arrayed by: Greg Lennon, Ph.D.			
DNA Sequencing by: Washington University Genome Sequencing Center found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbr/image/image.html			
Seq primer: -40P from Glico			
High quality sequence stop: 453.			
FEATURES			
Source			
1	(bases 1 to 638)		
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="txon:9606"			
/clone=IMAGE:2248878"			
/sex="male"			
/dev_stage="adult"			
/lab_host="DH10B"			
/clone.lib="NCI CGAP Pr28"			
/note="Organ: prostate; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloning vector 985608-986739, 1101192-1101959, and 121728-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."			
ORIGIN			
Query Match	59.8%	Score 613.8; DB 1; Length 638;	
Best Local Similarity	98.6%	Pred. No. 1.2e-156	
Matches	629;	Conservative 0; Mismatches 8; Indels 1; Gaps 1;	
Qy	391	GATGTCATCACATGATCCAAAGACAATGTC-AAGATGCAATGATCACT	449
Db	638	GATGTCATCACATGATCCAAAGACAATGTCATGTCATAGATGCGATGATCACT	579
450	GCTGGAGCTCACAAACACCTCTGATTAATCATGACTCTCTGCTCTCAAGAGTG	509	
RESULT 9			
LOCUS	CN645427	CN645427	CN645427
DEFINITION	ILLUMIGEN MCQ 23989 Katze_MMSP Macaca mulatta mRNA	959 bp	mRNA linear EST 13-MAY-2004
ACCESSION	CN645427	CN645427	ILLUMIGEN MCQ 23989 Katze_MMSP Macaca mulatta cDNA clone TRGE (HS_385086), mRNA sequence.
VERSION	CN645427.1	GI:47158870	
KEYWORDS			
SOURCE			
ORGANISM	Macaca mulatta (rhesus monkey)		
COMMENT			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Euarchoptoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.			
REFERENCE			
AUTHORS			
1	(bases 1 to 959)		
Magnes,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Asby,M.B., Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and Iadonato,S.P.			
TITLE			
JOURNAL			
PUBLMED			
COMMENT			
Contact: C. Magnes			
Illumigen Biosciences Inc.			
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA			
Tel: 2063780400			
Fax: 2063780408			
Email: cmagnes@illumigen.com			
Sequenced on 2004.02.24. 794 Q20 bases.			
PCR Primers			
FORWARD: CCCTCACTAAGGGACAAA			
BACKWARD: CACTTAGGCGGAAATGGGTA			
Insert Length: 959 Std Error: 0.00			

Plate:	CL000136	row:	G	column:	03
Seq primer:	CCCTCACTAAGGGACACAA				
POLY(A) Yes:					
FEATURES		Location/Qualifiers			
source	1. . 959	/organism="Macaca mulatta"			
		/mol_type="mRNA"			
		/strain="Indian"			
		/db_xref="taxon:9544"			
		/clone_id="IBI0W:10243"			
		/sex="male"			
		/cell_type="mononuclear lymphocyte"			
		/dev_stage="adult"			
		/lab_host="E. coli" SOLR			
		/clone lib="Katzze:MMSP"			
		/note="organ: spleen; vector: Uni-ZAP XR; Site 1: EcoRI I; Site 2: Xba I; Created from Stratagene ZAP-cDNA Synthesis Kit (Catalog #200400) and ZAP-cDNA Gigapack III Gold Cloning Kit (Catalog #200450)"			
ORIGIN					
Query Match	58.9%	Score 605.2;	DB 7;	Length 959;	
Best Local Similarity	81.3%	Pred. No. 2.9e-154;			
Matches	759;	Conservative 0;	Mismatches 78;	Indels 96;	Gaps 1;
Db	1	GATACATGGCGAAGAACGAGAACAGCAGCACRAAGGTCTGAAATCCAGAGGGRAACCAT	248		
Qy	189	GATACATGGCGAAGAACGAGAACAGCAGCACRAAGGTCTGAAATCCAGAGGGRAACCAT	248		
Db	249	GAAAGACTAACACACATACITGAATTAGCTGGTTAACCGTGCAGAAGAAGTCACTGGA	308		
Qy	61	GAAAGACTAACACACATACATGAATTAGCTGGTTAACCGTGCAGAAGAAGTCACTGGA	120		
Db	309	CAAAGAACACAGATGTATCGTCAGACATGAGATAATAAACCGAGGTGTAGAATTA	368		
Qy	121	TAAGAGCAGCAGTAGTCTCAGACAGCAGATAATAGAATGGTGTGATCANGAAT	180		
Db	369	TATCTTCCCTCAATAAGAGGGAT-----	395		
Qy	181	TATCTTCCCTCAATAAGAGAGATGTCACCAACAGTGGATCCCAAAGACAGTTTCAAA	240		
Qy	396	-	395		
Db	241	AGACCCAATGATGTCACCACAGTGATCCCAAAGCGAATTATCAGAAGATGGAGATGA	300		
Qy	396	--CATCACAAATGGATCCCAAAGACATTTGTCAAAAGATGCAATGATACTACTGCT	452		
Db	301	TGACACCAACAGTGGATCCCAAAGACATTTGAGAATGTCAAATGATGCCAACTGCT	360		
Qy	453	CGAGCTCACAAACACCTCTGCATTAATGATGCTTCTCTGCTCTGCTGAGCTGTGCT	512		
Db	361	CGACGTCAACAAACACCTCTGCATTAATGATGCTTCTCTGCTGAGCTGTGAGGAGGT	420		
Qy	513	CTATTGCTCATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	572		
Db	421	CTATTGCTCATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480		
Qy	573	GAATCTATAAGAGACGGACAGACAGGGCATCTTCTCATGGTTATGTCCTA	632		
Db	481	GAGATGCTAACAGAGACGGACAGACAGGGCATCTTCTCATGGTTATGTCCTA	540		
Qy	633	GAAGGCCTCTTGAGGATCTGTTGGCTCTTCTGGCTTGGCCATTCTCAGTC	692		
Db	541	GAAGGTGTTCTTGAGGATCTGTTGGCTCTTCTGGCTTGGCTTCTC	600		
Qy	693	ATGTGTTACTATCTCATATGTTAACTGAGGTCTGCTGCTGCTGCTGCTGCTG	752		
Db	601	ACCTCACTCTGTTAACTGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	660		
Qy	753	ACCTCACTCTGTTAACTGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	812		
Db	661	ACCTCACTCTGTTAACTGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG	720		
ORIGIN					
Query Match	57.5%	Score 590.2;	DB 2;	Length 703;	
Best Local Similarity	97.3%	Pred. No. 3.5e-150;			
Matches	621;	Conservative 0;	Mismatches 14;	Indels 3;	Gaps 2;
Db	391	GATGTCATCACATGGATCCAAAGACATGTCATGGTCATGGTCATGGTCATGGTC	450		
Qy	53	GATGTCATCACATGGATCCAAAGACATGTCATGGTCATGGTCATGGTCATGGTC	111		
Db	451	CTGCACTCACAAACACCTCTGCATATGATGACTCTCTGCTCTCAAGGTG	510		
Db	112	CTGCACTCACAAACACCTCTGCATATGATGACTCTCTGCTCTCAAGGTG	171		

QY 511 GTCATTGCGCATCATCACCTGCTGCTGAGAACGCCCTTCTGCACATGGA 570 /db_xref="taxon: 9606"
 Db 172 GTCATTGCGCATCATCACCTGCTGCTGAGAACGCCCTTCTGCACATGGA 231 /clone="IMAGE:240183"
 QY 571 GAGAAATCATACAGACGGTGCAAGAGGCCATCTTCCATCGTTATGRC 630 /tissue_type="2' pooled tumors (clear cell type)"
 Db 232 GAGAAATCATACAGACGGTGCAAGAGGCCATCTTCCATCGTTATGRC 291 /lab_host="DH10B"
 QY 631 TAGAGGCGCTCTGAGGATCTACTGCGCTTCTCGGTGCGCATTCAGTC 690 /clone lib="NCI CGAP Kidz2"
 Db 292 TAGAGGCGCTCTGAGGATCTACTGCGCTTCTCGGTGCGCATTCAGTC 351 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI CGAP Kidz was
 prepared, and ss circles were made in vitro. Following HAP
 purification, thi DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneIDs 1323912-1325831, 1471368-1472903 and
 1492104-1493255). Subtraction by Bento Soares and M.
 Fatima Bonaldo."
 Db 691 TCTGTGCTACTTCTATCATATTGATAACAGGAATGCCACGGTTCAACCAGGCAACAGA 750
 Db 352 TCTGTGCTACTTCTATCATATTGATAACAGGAATGCCACGGTTCAACCAGGCAACAGA 411
 QY 751 GAACCTCACTCTGTAATACATGAGGAATGCCACGGTTCAACCAGGCAACAGA 810
 Db 412 GAACCTCACTCTGTAATACATGAGGAATGCCACGGTTCAACCAGGCAACAGA 471
 Db 811 CATGTTCCACAGCTCCCTCCASCAACCAATTAGCSCCTGCTATAGTAGACATCT 870
 Db 472 CATTGTTCAACAGCTCCAGCAACCCAATTAGCSCCTGCTATAGTAGACAGCT 531
 QY 871 GCGGCTCTAGGCTGTCCTCTCTAGTGTCTTAACTGATAACTGCGTGAAGCT 930
 Db 532 GCGGCTCTAGGCTGTCCTCTCTAGTGTCTTAACTGATAACTGCGTGAAGCT 591
 QY 931 TCATTTACAAGCCTGAGAGCAGCTCTTGCTAGTGTGATATGTCG - TGTGTT 988
 Db 592 TCTTTTACAGCGCTCTGAGAGCAGCTCTTGCTAGTGTGATATGTCG - TGTGTT 651
 QY 989 TCCCTAATAGCAAAATAATTAAAMATGAAAGT 1026
 Db 652 CCCGTAATAGCAAAATAATTAAAMATGAAAGT 689
 RESULT 11
 A176834/c
 LOCUS A176834 629 bp mRNA linear EST 21-DEC-1999
 DEFINITION wJ03h04.x1 NCI CGAP Kidz12 Homo sapiens cDNA clone IMAGE:2401783 3',
 mRNA sequence.
 ACCESSION A176834
 VERSION A176834.1 GI:5235343
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Human
 Hukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchoptoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 629)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Title Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 DNA Library Preparation: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmer-Buck, M.D., Ph.D.
 Tissue Procurement: M. Bento Soares, Ph.D.
 DNA sequencing Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the T.M.A.G.B. Consortium/LIN at:
 www-bio.llnl.gov/lbri/image/image.html
 Insert Length: 1658 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 428.
 FEATURES source
 1. .629
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /mol_type="mRNA"
 RESULT 12
 CA449324/c 700 bp mRNA linear EST 08-Nov-2002
 LOCUS CA449324
 DEFINITION UI-H-E1-ayt-k-17-0-UI-81 NCI CGAP_E1 Homo sapiens cDNA clone
 UI-H-E1-ayt-k-17-0-UI 3', mRNA sequence.
 ACCESSION CA449324
 VERSION CA449324.1 GI:24813744

FEATURES	SOURCE	EST.
source	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbbs-remail.nih.gov Tissue Procurement: Dr. Jose Marcuende DNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu The following repetitive elements were found in this cDNA sequence: 1-29', >AT rich#low_complexity Seq primer: M13 FORWARD POLYA=Yes.	
FEATURES	Location/Qualifiers	
source	1. . 700 <organism="Homo sapiens" <mol_type="mRNA" <db_xref="taxon:9606" <clone="UI-H-EL1-ayt-k-17-0-UI" <tissue="Lypar-Chondrosarcoma" <dev_stage="adult" <lab_host="DH10B" (Life Technologies)" <clone_lib="NCI-CGAP_E11" <note="Organ: Left Pelvis; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI-CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dTT)18 tail. The sequence tag for this library is ACGTTGCAC. TAG TISSUE=chondrosarcoma TAG LIB=UI-H-EL1 TAG SEQ=ACGTTGCAC"	
ORIGIN		
Query Match	56.9%	Score 584; DB 6; length 700;
Best Local Similarity	95.9%	Pred. No. 1.7e-148;
Matches	629; Conservative 0; Mismatches 5; Indels 22; Gaps 2;	
QY	391 GATGTCATCAGATGGCCAAAGAACATTGTCAAGATGCAAT-----	438
Db	661 GATGTCATCAGATGGCCAAAGAACATTGTCAAGATGCAAT-----	602
QY	439 -----GATACTACTCTGCACTCTGCAACACCTTGATGACCTC	489
Db	601 TTTCCTTGTAGATCACTACTCTGCACTCTGCAACACCTTGATGACCTC	542
QY	490 CTCCCTGCTCC-AAGAGTGGCTATTGCCCACATGCCAATGCAATGTGCAA	548
Db	541 CTCCTGCTCCNAAGAGTGGCTATTGCCCACATGCCAATGCAATGTGCAA	482
QY	549 AACGGCTTCTCTGCAATGGAGAGAATCTAACGACGGCTCACAGGGCCATC	608
Db	481 AACGGCTTCTGCTGCAATGGAGAGAATCTAACGACGGCTCACAGGGCCATC	422
QY	609 TTCTCATCGGTATGCTCTAGAGCGCTCTGAGGAGCTAGTGGCTCTTC	668
FEATURES	Location/Qualifiers	
source	1. . 582 <organism="Homo sapiens" <mol_type="mRNA" <db_xref="taxon:9606" <clone="IMACB:3133257" <lab_host="DH10B" <clone_lib="NCI-CGAP_Kid11" <note="Organ: kidney; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; plasmid DNA from the normalized library NCI-CGAP_Kid11 was prepared, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA	
Db	421 TTCTCTCATGGTATGTCCTAGAGCTCTGGAGCTAGTGGCTTC 362	
QY	659 TGGTTGGCCATTCTGGTCTCATGTTGTTACTATCTATTGTTAACGTT 728	
Db	361 TGGTTGGCCATTCTGGTCTCATGTTGTTACTATCTATTGTTAACGTT 302	
QY	729 TCAACAGTGGCAGAGAACCTCACTGTAACTAACATGAGGAATGCCACGG 788	
Db	301 TTCAACAGTGGCAGAGAACCTCACTGTAACTAACATGAGGAATGCCACGG 242	
QY	789 CGATTCAGCACCAATCTCCATGTTCCAGCTCTCCAGCCACCAAATGCCACGG 848	
Db	241 CGATTCAGCACCAATCTCCATGTTCCAGCTCTCCAGCCACCAAATGCCACGG 182	
QY	849 CCTGCTTATGTTGAGACATCTGGGCTCTAGCCCTTCTCTAGTGTCTTAA 908	
Db	181 CCTGCTTATGTTGAGACAGCCCTGGGCTCTAGCTCTCCCTCTCTAGTGTCTTAA 122	
QY	909 TCAGATACTGCTGGAGGCCCTCATTTACAGCCCTGAGCTCTCTGTGCTGT 968	
Db	121 TCAGATACTGCCTGGAGACCTCTATTACAGCCCTGAGCAGCTCTGTGCTGT 62	
QY	969 TGATTAATGGTGTGTTCCGTAATAAGCAAAATAATTAAAGATGAAA 1024	
Db	61 TGATTAATGGTGTGTTCCGTAATAAGCAAAATAATTAAAGATGAAA 6	
RESULT	BB26754/c	
LOCUS	BB26754	582 bp mRNA linear EST 14-JUL-2000
DEFINITION	BB26754.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:311257_3', similar to gb:WJ2331 T-CSU RECEPTOR GAMMA CHAIN C REGION (HUMAN); mRNA Sequence.	
ACCESSION	BB26754	
VERSION	BB26754.1	GI:9200330
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo Sapiens	
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbbs-remail.nih.gov	
FEATURES	Location/Qualifiers	
source	Christopher Moskaluk, M.D., Ph.D., Michael R. Bennett-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I-M.A.G.E. Consortium/LINL, send email to: info@image.lnl.gov Seq primer: -40bp from Gibco High quality sequence stop: 447.	

LOCUS BP681238 36215502F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296504 5', linear EST 21-DEC-2000
DEFINITION mRNA
ACCESSION BF681238 371 TCTTCCTCCATAAGACGGATGTCATCACATTGATCCCAGAACATTGTTCAAG 43
VERSION BF681238.1 364 CTTCCTCCATAAGACGGATGTCATCACATTGATCCCAGAACATTGTTCAAG 42
KEYWORDS EST. 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
SOURCE Homo sapiens (human) 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
ORGANISM Homo Sapiens 491 TCTGCTCTCAGTGTGCTA-TTTGCCATCATCACCTCTGCAATTACATGTACCTC 490
TITLE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
AUTHORS Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
JOURNAL NIH-MGC http://mgc.nci.nih.gov/ 491 TCTGCTCTCAGTGTGCTA-TTTGCCATCATCACCTCTGCAATTACATGTACCTC 490
COMMENT Unpublished (1999) 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
Contact: Robert Strausberg, Ph.D. 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
Email: cgapbs@mail.nih.gov 491 TCTGCTCTCAGTGTGCTA-TTTGCCATCATCACCTCTGCAATTACATGTACCTC 490
Tissue Procurement: CLONETECH Laboratories, Inc. 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
Procurement: CLONETECH Laboratories, Inc. 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
CDNA Library Preparation: CLONETECH Laboratories, Inc. 491 TCTGCTCTCAGTGTGCTA-TTTGCCATCATCACCTCTGCAATTACATGTACCTC 490
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN) 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
DNA Sequencing by: Incyte Genomics, Inc. 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
Clone distribution: MGC clone distribution information can be 491 TCTGCTCTCAGTGTGCTA-TTTGCCATCATCACCTCTGCAATTACATGTACCTC 490
found through the I.M.A.G.E. Consortium/LILN at: http://image.liln.gov 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
Plate: LICH149 **row:** c **column:** 01 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
High quality sequence stop: 673.
FEATURES
source
1 .719 location/Qualifiers
1 .719 /organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon:9606"
/clone="IMAGE:4286504"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgcgcgc); Site 2: SfiI
(ggcgtttatggcc), 5', and 3', adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTAGGCC-3'
and 3' adaptor sequence:
5'-ATTCTGAGGCCGGCGATATG-3T(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14115 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
ORIGIN
Query Match 55.5% Score 569.8; DB 2; Length 719;
Best Local Similarity 94.6%; Pred. No. 1.4e-144; 8;
Matches 678; Conservative 0; Mismatches 27; Indels 12; Gaps 8;
QY 11 TGGGCAAAATCAGGTTGGCCCAAGCAGCTTACATGATACAAAC 70 371 TCTTCCTCCATAAGACGGATGTCATCACATTGATCCCAGAACATTGTTCAAG 43
Db 5 TGGGCAAAATCAGGTTGGCCCAAGCAGCTTACATGATACAAAC 64 364 CTTCCTCCATAAGACGGATGTCATCACATTGATCCCAGAACATTGTTCAAG 42
QY 71 TTGATGCAAGCTGGACATACCTTGTCTCTTGACAAATTTCCTCTGCAATTGCTGAACAAAGC 130 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
Db 65 TTGATGCAAGCTGGACATACCTTGTCTCTTGACAAATTTCCTCTGCAATTGCTGAACAAAGC 124 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
QY 131 TCCAGCAAGCTGGACATACCTTGTCTCTTGACAAATTTCCTCTGCAATTGCTGAACAAAGC 190 491 TCTGCTCTCAGTGTGCTA-TTTGCCATCATCACCTCTGCAATTACATGTACCTC 490
Db 125 TCCAGCAAGCTGGACATACCTTGTCTCTTGACAAATTTCCTCTGCAATTGCTGAACAAAGC 183 431 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 491
QY 191 TACATGGCAAGAAGAAGACGACACGATTGGATCCAGGGAAACCCATGA 250 424 ATGAAATGATACACTACTGCTGAGTCACAAACACCTCTGCAATTACATGTACCTC 483
Db 244 AGACTTAATGAGACATACATGAATTAGCTGGTTACGGTCCAGGAGGAACTGGACA 303 184 TACATGGCAAGAAGAAGACGACACGATTGGATCCAGGGAAACCCATGA 243
QY 3.1 AAGACACAGATGTTGCTGAGACATGAGATAATRAAACGGAGTTGATCAAGAATT 370

Copyright (C) 1993 - 2005 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: December 10, 2005, 17:49:47 ; Search time 664 Seconds
(without alignment(s))
10308.192 Million cell update

XX	Sequence 1027 BP; 307 A; 232 C; 200 G; 288 T; 0 U; 0 Other;	Db	961 TTGTAGTGAATTATGTTGGTGTCTTCGGTATAAGCAAAATAAATTAAG 1020
SQ	Query Match 100.0%; Score 1027; DB 4; Length 1027; Best Local Similarity 100.0%; Pred. No. 4, 3e-290; Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY	1021 AAAAGTT 1027
QY	1 GGGCAGAGTTGGCAAAAMATCAGGATTGTTCCCGAACAGCTTACATAA 60	Db	1021 AAAAGTT 1027
Db	1 GGGCAGAGTTGGCAAAAMATCAGGATTGTTCCCGAACAGCTTACATAA 60	RESULT 2	ADB75580
QY	61 GATAAACACTGTGTCAGAGTTGCCAACACTATTTCCTCTGAT 120	ID	ADB75580 standard; cDNA; 1027 BP.
Db	61 GATAAACACTGTGTCAGAGTTGCCAACACTATTTCCTCTGAT 120	XX	XX
QY	121 GAAACRAAAGCTCCAGAGAGTGGACATACCTTGCTCTGAGAAATTTCCTGAT 180	AC	ADB75580;
Db	121 GAAACRAAAGCTCCAGAGAGTGGACATACCTTGCTCTGAGAAATTTCCTGAT 180	XX	XX
QY	181 GTTATTAGATACATGGCAAGAAGAAGAGGAAACACGATCTGGATCCAGAGGG 240	DE	04-DEC-2003 (first entry)
Db	181 GTTATTAGATACATGGCAAGAAGAAGAGGAAACACGATCTGGATCCAGAGGG 240	XX	Prostate cancer marker cDNA.
QY	241 AACACCATGAGACTAACGACACATACATGAATTAGCTGTTAACGGTGGCCAGAAAG 300	XX	KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
Db	241 AACACCATGAGACTAACGACACATACATGAATTAGCTGTTAACGGTGGCCAGAAAG 300	OS	XX
QY	301 TCACTGACAAAGAACACAGATGTCAGAACATGAGATAAAGAGGATGT 360	XX	Homo sapiens.
Db	301 TCACTGACAAAGAACACAGATGTCAGAACATGAGATAAAGAGGATGT 360	PN	XX
QY	361 CGAAAGATTATCTCCATAAGACCGATCACAAATGGATCCAAAGAACAT 420	PD	WO2003009814-A2.
Db	361 CGAAAGATTATCTCCATAAGACCGATCACAAATGGATCCAAAGAACAT 420	XX	06-FEB-2003.
QY	421 TGTGCAAAAGTGCAATGATACATGACTACTGTGCACTAACAAACCTTGATATTAC 480	XX	XX
Db	421 TGTGCAAAAGTGCAATGATACATGACTACTGTGCACTAACAAACCTTGATATTAC 480	PR	25-JUL-2002; 2002HO-US023913.
QY	481 ATGTAACCTCTCTCTGTCTGCCTCAAGAGGTGTTGCTTGCAGTCACAAACCTGCTG 540	XX	XX
Db	481 ATGTAACCTCTCTCTGTCTGCCTCAAGAGGTGTTGCTTGCAGTCACAAACCTGCTG 540	PR	25-JUL-2001; 2001US-0314356P.
QY	541 CTTAGAGAAAGGTTCTGCAATGGAGAACATACAGACGGTGGCICAGGA 600	XX	PR 05-MAR-2002; 2002US-032158P.
Db	541 CTTAGAGAAAGGTTCTGCAATGGAGAACATACAGACGGTGGCICAGGA 600	PA	(MILL-) MILLENNIUM PHARM INC.
QY	601 GGCCATCTTCTCATCGGTATGCTCTAGAACGGTTCTGGAGTCTAGTGGC 660	PI	Schlegel R, Monahan JE, Gannavarapu M, Gorbatcheva B,
Db	601 GGCCATCTTCTCATCGGTATGCTCTAGAACGGTTCTGGAGTCTAGTGGC 660	XX	Pi Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
QY	661 TTCTCTCTGGGTTGGCCATTCACTGCTCATGCTGTTCTGAGGGCTAGTGGC 720	DR	DR WPI; 2003-248033/24.
Db	661 TTCTCTCTGGGTTGGCCATTCACTGCTCATGCTGTTCTGAGGGCTAGTGGC 720	XX	New nucleic acid molecule, useful for diagnosing or treating prostate cancer.
QY	721 TACACGTTAACACAGTGGCACAGAACCTACTGTAAACATGAGGAAT 780	PT	PT Disclosure; SEQ ID NO 404; 99pp; English.
Db	721 TACACGTTAACACAGTGGCACAGAACCTACTGTAAACATGAGGAAT 780	XX	The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB7517-ADB7531 represent marker cDNA and proteins. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.
QY	781 AGCCACGGGATCTCCAGCACATCTCAGTTCCACAGCTCTCGGCAACC 840	XX	Sequence 1027 BP; 307 A; 232 C; 200 G; 288 T; 0 U; 0 Other;
Db	781 AGCCACGGGATCTCCAGCACATCTCAGTTCCACAGCTCTCGGCAACC 840	QY	Query Match 100.0%; Score 1027; DB 10; Length 1027; Best Local Similarity 100.0%; Pred. No. 4, 3e-290; Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	841 AAATAGCGCTCTGATAGTGTAGACATCCCTCGGCTCTACGCTCTAGTG 900	Db	1 GGGCAGAGTTGGCAAAATCAAGGATTGTTCCCGAACAGCTTACATAA 60
Db	841 AAATAGCGCTCTGATAGTGTAGACATCCCTCGGCTCTACGCTCTAGTG 900	QY	901 TCTTTAATCGATAACTGCGTGAAGCCITCTTCACTTACKGCCCTGAGCAGCTCT 960
QY	901 TCTTTAATCGATAACTGCGTGAAGCCITCTTCACTTACKGCCCTGAGCAGCTCT 960	Db	901 TCTTTAATCGATAACTGCGTGAAGCCITCTTCACTTACKGCCCTGAGCAGCTCT 960
QY	961 TTGCTAGTGTGATTATGGGGTTTCCGATAAGCAAAATAATTAAAATG 1020	QY	61 GATAACATGTCAGAGTGGTCCCGAACCCATTTCTCTCAATTG 120

DT 18-NOV-2004 (first entry)
 XX
 DE Human. PRO cDNA sequence SEQ ID NO:838.
 XX
 KW human; PRO; immune related disease; inflammatory immune response;
 KW immune response stimulation; antiallergic; antiarthritic;
 KW antidiabetic; antiinflammatory; antipsoriatic;
 KW antitussive; antihypertensive; CNS; dermatological; gastrointestinal;
 KW haemostatic; hepatotrophic; immunostimulant; immunosuppressive; muscular;
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
 KW virucide; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004039956-A2.
 XX
 PR 28-OCT-2003; 2003WO-US034381.
 XX
 PR 29-OCT-2002; 2002US-0422472P.
 XX
 DA (GETH) GENENTECH INC.
 XX
 PT Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX DR WPI; 2004-376182/35.
 XX DR P-PSDB; ADB54863.

PT New PRO poly nucleotides and polypeptides, useful in useful in diagnosing
 PT and treating an immune related disease, e.g. systemic lupus
 PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
 PT stimulating an immune response.

XX PS Claim 2; SEQ ID NO 838; 3009PP; English.

CC The present invention describes an isolated PRO nucleic acid (1). Also
 CC described: (1) a vector comprising (1); (2) a host cell comprising the
 CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
 CC antibody which specifically binds to a polypeptide of (4); (7) a
 CC composition of matter comprising a polypeptide of (4), an agonist or
 CC antagonist of the polypeptide or an antibody that binds to the
 CC polypeptide in combination with a carrier; (8) an article of manufacture
 CC comprising a container, a label on the container and a composition of
 CC comprising (7); (9) a method of treating an immune related disease in a
 CC mammal; (10) a method for determining the presence of a PRO polypeptide
 CC in a sample suspected of having the polypeptide; (11) a method of
 CC diagnosing an immune related disease or an inflammatory immune response
 CC in mammal; (12) a method of identifying a compound that inhibits or
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide
 CC and (13) a method of stimulating the immune response in a mammal. The
 CC PRO sequences have antiallergic, antianaemic, antiarthritic,
 CC antiasthmatic, antidiabetic, antinflammatory, antipsoriatic,
 CC antirheumatic, antidiabetic, CNS, dermatological, gastrointestinal,
 CC haemostatic, hepatotrophic, immunostimulant, immunosuppressive, muscular,
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 CC virucide activities, and can be used in gene therapy. The nucleic acid
 CC (1) and the encoded polypeptides, compositions, kits and methods are
 CC useful in diagnosing and treating an immune related disease and in
 CC stimulating an immune response. The present sequence represents a human
 CC PRO nucleotide sequence from the present invention.

XX Sequence 1027 BP; 307 A; 232 C; 200 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 1027; DB 13; Length 1027;
 Best Local Similarity 100.0%; Pred. No. 4.3e-290;
 Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGCGAAGGTTGGCAAAAMATCAAGGTATTGGTCGGGACAAAGCTTACATACA 60
 XX

RESULT 3
 ADP54862
 ID ADP54862 standard; cdna; 1027 BP.
 XX
 AC ADP54862;
 XX

RESUME

ADW44400

Qy	Sequence 1027	BP:	100.0%	Score	1027;	DB	14;	Length	1027;
Qy	GGCCAAAGCTGGCCAAAATCAAGGATTATGGCCGGACAAAGCTTATCATACA	1	100.0%	100.0%	Pred.	No.	4	3e-290;	Best Local Similarity
Db	GSGCAAGAGTTGGCCAAAATCAAGGATTATGGCCGGACAAAGCTTATCATACA	1	100.0%	100.0%	Mismatches	0;	0	Indels	Conservative
Qy	GATAAACACTGATGCGATGTTCCCAGACGCCACATTTCTTCCTCAATGCT	61	100.0%	100.0%	Gaps	0;	0	0	Mismatches
Db	GATRAACACTGATGCGATGAGTTCCCAGACGCCACATTTCTTCCTCAATGCT	61	100.0%	100.0%	Indels	0;	0	0	Indels
Qy	GTTTAGATACATGGCAGAAGAGAGAGACAGATCTGGATCCGGAGGG	181	100.0%	100.0%	Matches	1027;	0	0	Matches
Db	GTTTAGATACATGGCAGAAGAGAGAGACAGATCTGGATCCGGAGGG	181	100.0%	100.0%	Conservative	0;	0	0	Conservative
Qy	GTATTAGATACATGGCAGAAGAGAGAGACAGATCTGGATCCGGAGGG	241	100.0%	100.0%	Indels	0;	0	0	Indels
Db	GTATTAGATACATGGCAGAAGAGAGAGACAGATCTGGATCCGGAGGG	241	100.0%	100.0%	OS	0;	0	0	OS
Qy	AACACATGAGACTAACGACACATACATGAAATTAGCTGGTAACGGTGCAAGAAG	300	100.0%	100.0%	XX	0;	0	0	XX
Db	AACACATGAGACTAACGACACATACATGAAATTAGCTGGTAACGGTGCAAGAAG	300	100.0%	100.0%	XX	0;	0	0	XX
Qy	TCACTGGACAAAGACACAGATGATCGTCAGACATGAAATAAACACGAGTGAT	301	100.0%	100.0%	XX	0;	0	0	XX
Db	TCACTGGACAAAGACACAGATGATCGTCAGACATGAAATAAACACGAGTGAT	301	100.0%	100.0%	XX	0;	0	0	XX
Qy	CHAGAAATCTTCTCAATAGAGGGATCTACACAAATGATCCAAAGACAT	361	100.0%	100.0%	KW	0;	0	0	KW
Db	CHAGAAATCTTCTCAATAGAGGGATCTACACAAATGATCCAAAGACAT	361	100.0%	100.0%	cancer;	0;	0	0	cancer;
Qy	CAAGAAATTACTTCTCCTCAAATAAGAGGGATCTACACAAATGATCCAAAGACAT	420	100.0%	100.0%	ss.	0;	0	0	ss.
Db	CAAGAAATTACTTCTCCTCAAATAAGAGGGATCTACACAAATGATCCAAAGACAT	420	100.0%	100.0%	XX	0;	0	0	XX
Qy	TGTTCAAAGATGAAATGATGAACTACTACTGCTGAGCTCACAAACACTCTGATATTAC	421	100.0%	100.0%	Hom sapiens.	0;	0	0	Hom sapiens.
Db	TGTTCAAAGATGAAATGATGAACTACTACTGCTGAGCTCACAAACACTCTGATATTAC	421	100.0%	100.0%	XX	0;	0	0	XX
Qy	ATGCTACCTCTCTCTCTCTCAAGACTGCTGATTTGCCATCACCTCTGCTG	481	100.0%	100.0%	W02004016225-A2.	0;	0	0	W02004016225-A2.
Db	ATGCTACCTCTCTCTCTCAAGACTGCTGATTTGCCATCACCTCTGCTG	481	100.0%	100.0%	XX	0;	0	0	XX
Qy	CTTAGAAGACGGTTCTGCTGAAATGGAGAGAAATCAACAGACGCGTGGACAGGA	540	100.0%	100.0%	PD	0;	0	0	PD
Db	CTTAGAAGACGGTTCTGCTGAAATGGAGAGAAATCAACAGACGCGTGGACAGGA	540	100.0%	100.0%	XX	0;	0	0	XX
Qy	GSCCTCTTCTCAATCGTTGCTTCTAGGATCTGCTGCTGCTGCTG	541	100.0%	100.0%	PP	0;	0	0	PP
Db	GSCCTCTTCTCAATCGTTGCTTCTAGGATCTGCTGCTGCTGCTG	541	100.0%	100.0%	XX	0;	0	0	XX
Qy	CTTAGAAGACGGCTTCGCTGAAATGGAGAGAAATCAACAGACGCGTGGACAGGA	600	100.0%	100.0%	PR	0;	0	0	PR
Db	CTTAGAAGACGGCTTCGCTGAAATGGAGAGAAATCAACAGACGCGTGGACAGGA	600	100.0%	100.0%	XX	0;	0	0	XX
Qy	GCGCTCTTCTCAATCGTTGCTTCTAGGATCTGCTGCTGCTGCTG	601	100.0%	100.0%	PR	0;	0	0	PR
Db	GCGCTCTTCTCAATCGTTGCTTCTAGGATCTGCTGCTGCTGCTG	601	100.0%	100.0%	XX	0;	0	0	XX
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	661	100.0%	100.0%	WPI;	0;	0	0	WPI;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	661	100.0%	100.0%	XX	0;	0	0	XX
Qy	TAACGGTTTCAACACAGTGGGGCAACAGAAACCTACTCTGTTATAACATGGGAT	721	100.0%	100.0%	PS	0;	0	0	PS
Db	TAACGGTTTCAACACAGTGGGGCAACAGAAACCTACTCTGTTATAACATGGGAT	721	100.0%	100.0%	XX	0;	0	0	XX
Qy	AGCCACGGGAGATCTCCACCAATCTCCCTGTTAACGAGCTCCCTCCAGGACACC	781	100.0%	100.0%	PT	0;	0	0	PT
Db	AGCCACGGGAGATCTCCACCAATCTCCCTGTTAACGAGCTCCCTCCAGGACACC	781	100.0%	100.0%	XX	0;	0	0	XX
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	840	100.0%	100.0%	Claim 1; SEQ ID NO 23; 319pp; English.	0;	0	0	Claim 1; SEQ ID NO 23; 319pp; English.
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	840	100.0%	100.0%	XX	0;	0	0	XX
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	841	100.0%	100.0%	New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or	0;	0	0	New antibody that binds to a tumor-associated antigenic target (TAT) polypeptide, useful for preparing a composition for diagnosing or
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	841	100.0%	100.0%	PT treating cancer.	0;	0	0	PT treating cancer.
Qy	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	901	100.0%	100.0%	XX	0;	0	0	XX
Db	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	901	100.0%	100.0%	CC	0;	0	0	CC
Qy	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	901	100.0%	100.0%	CC	0;	0	0	CC
Db	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	901	100.0%	100.0%	CC	0;	0	0	CC
Qy	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	901	100.0%	100.0%	CC	0;	0	0	CC
Db	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	901	100.0%	100.0%	CC	0;	0	0	CC
Qy	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	100.0%	100.0%	CC	0;	0	0	CC
Db	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	100.0%	100.0%	XX	0;	0	0	XX
Qy	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	100.0%	100.0%	Sequence 1395	0;	0	0	Sequence 1395
Db	TTCTTAATCGATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	961	100.0%	100.0%	BP:	405	A;	324	C;
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	BP:	405	A;	286	G;
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	BP:	405	A;	286	T;
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	BP:	405	A;	286	U;
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	BP:	405	A;	286	Other;
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Best Local Similarity	99.8%	;	Score	1013.8;
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Best Local Similarity	99.8%	;	DB	12;
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Length	1395;	;	Length	1395;
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Matches	1015;	;	Matches	1015;
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Conservative	0;	;	Conservative	0;
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Mismatches	2;	;	Mismatches	2;
Qy	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Indels	0;	;	Indels	0;
Db	AAATGCGCTGCTATAGCTAGACATCTGCAGCTTAGCTGCTCTCTAGTG	900	100.0%	100.0%	Gaps	0;	;	Gaps	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	RESULT 5	0;	;	RESULT 5	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	IDL06443	0;	;	IDL06443	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	standard; cDNA; 1395 BP.	0;	;	standard; cDNA; 1395 BP.	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	ADL06443;	0;	;	ADL06443;	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	AC	0;	;	AC	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	XX	0;	;	XX	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	DT	0;	;	DT	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	20-MAY-2004 (first entry)	0;	;	20-MAY-2004 (first entry)	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	Human tumour-associated antigenic target (TAT) cDNA sequence #23.	0;	;	Human tumour-associated antigenic target (TAT) cDNA sequence #23.	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	Human; tumour-associated antigenic target; TAT; cell death; tumour;	0;	;	Human; tumour-associated antigenic target; TAT; cell death; tumour;	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	cancer; cyostatic; gene; ss.	0;	;	cancer; cyostatic; gene; ss.	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	PA	0;	;	PA	0;
Qy	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	(GBETH) GENENTECH INC.	0;	;	(GBETH) GENENTECH INC.	0;
Db	CAAGAGTTGGCCAAAATCAAGGATTGGCCCCGAGACAGCTTACAGTG	63	100.0%	100.0%	PI	0;	;	PI	0;
Qy	Spencer SD, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;	540	100.0%	100.0%	Spencer SD, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;	0;	;	Spencer SD, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;	0;
Db	Spencer SD, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;	540	100.0%	100.0%	XX	0;	;	XX	0;
Qy	WPI; 2004-257144/24.	540	100.0%	100.0%	DR	0;	;	DR	0;
Db	WPI; 2004-257144/24.	540	100.0%	100.0%	XX	0;	;	XX	0;
Qy	CTAGCTCTCTCTCTCTCAAGACTGCTGATTTGCCATCACCTCTGCTG	540	100.0%	100.0%	PS	0;	;	PS	0;
Db	CTAGCTCTCTCTCTCTCAAGACTGCTGATTTGCCATCACCTCTGCTG	540	100.0%	100.0%	XX	0;	;	XX	0;
Qy	CTAGCTCTCTCTCTCTCAAGACTGCTGATTTGCCATCACCTCTGCTG	540	100.0%	100.0%	PT	0;	;	PT	0;
Db	CTAGCTCTCTCTCTCTCAAGACTGCTGATTTGCCATCACCTCTGCTG	540	100.0%	100.0%	XX	0;	;	XX	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	PT treating cancer.	0;	;	PT treating cancer.	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	XX	0;	;	XX	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanized antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces a cell to which it binds. The antibody is useful for preparing a composition for diagnosing or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.	0;	;	The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polynucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanized antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces a cell to which it binds. The antibody is useful for preparing a composition for diagnosing or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	XX	0;	;	XX	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	CC	0;	;	CC	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	CC	0;	;	CC	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	CC	0;	;	CC	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	CC	0;	;	CC	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	CC	0;	;	CC	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	XX	0;	;	XX	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Sequence 1395	0;	;	Sequence 1395	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	BP:	405	A;	324	C;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	BP:	405	A;	286	G;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	BP:	405	A;	286	T;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	BP:	405	A;	286	U;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	BP:	405	A;	286	Other;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Best Local Similarity	99.8%	;	Score	1013.8;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Best Local Similarity	99.8%	;	DB	12;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Length	1395;	;	Length	1395;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Matches	1015;	;	Matches	1015;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Conservative	0;	;	Conservative	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Mismatches	2;	;	Mismatches	2;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Indels	0;	;	Indels	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Gaps	0;	;	Gaps	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	RESULT 5	0;	;	RESULT 5	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	IDL06443	0;	;	IDL06443	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	standard; cDNA; 1395 BP.	0;	;	standard; cDNA; 1395 BP.	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	ADL06443;	0;	;	ADL06443;	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	AC	0;	;	AC	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	XX	0;	;	XX	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	20-MAY-2004 (first entry)	0;	;	20-MAY-2004 (first entry)	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Human tumour-associated antigenic target (TAT) cDNA sequence #23.	0;	;	Human tumour-associated antigenic target (TAT) cDNA sequence #23.	0;
Qy	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	Human; tumour-associated antigenic target; TAT; cell death; tumour;	0;	;	Human; tumour-associated antigenic target; TAT; cell death; tumour;	0;
Db	TTCTTCGGTTGGCCATTCTAGTCTCATGTTCTATGTA	720	100.0%	100.0%	cancer; cyostatic; gene;				

Db 499 ||||| ACAAGCTCCAGAGGTGGACATACCTTGTCTCTGAGAAATTTCCTGATGT 559
 Kv ||||| Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 Qy 184 ATTAGATACATTCGAAGAAGAGAACACAGATTCTGGAACTCCAGGGGGAC 243
 Db 559 ATTAGATACATTCGGCAAGAACAGAGAACACAGATTCTGGAACTCCAGGGGGAC 618
 Kv ||||| KW
 Qy 244 ACCATGAAGACTAACGACATACATGAATTAGTGTTAAGGTGCCAGAACATCA 303
 Db 619 ACCATGAAGACTAACGACATACATGAATTAGTGTTAAGGTGCCAGAACATCA 678
 Kv 304 CTGGCAAGAACAGACAGATGTTCTCAGCATGGAATAAACCGGAGTGTCAA 363
 Db 679 CTGGCAAGAACAGACAGATGTTCTCAGCATGGAATAAACCGGAGTGTCAA 738
 Kv 364 GAAATTATCTTCCTCCAATAAGAGGGATCTCACATGGAATAAACCGGAGTGTCAA 423
 Db 739 GAAATTATCTTCCTCCAATAAGAGGGATCTCACATGGAATAAACCGGAGTGTCAA 798
 Qy 424 TCAAAAGATGCAAATGATACATGCTGGAGTCACAAACACTCTGCATATTACAG 483
 Db 799 TCAAAAGATGCAAATGATACATGCTGGAGTCACAAACACTCTGCATATTACAG 858
 Kv 484 TACCTCTCTCTCTCAAGAGTGGTTATTGCCCATACTCTGCTGCTGCTGCT 543
 Db 859 TACCTCTCTCTGCTCAGAGTGGTTATTGCCCATACTCTGCTGCTGCTGCT 918
 Kv 544 AGAAGAACGGGTTCTGCTGCAATGAGAACTCATAAAGACOGGTGSCAACAGGGC 603
 Db 919 AGAAGAACGGGTTCTGCTGCAATGAGAACTCATAAAGACOGGTGSCAACAGGGC 978
 Qy 604 CATCTTCTCCATGGTTATGCTCTAGAGCTCTCTGAGATCTAGTGGCTT 663
 Db 979 CATCTTCTCCATGGTTATGCTCTAGAGCTCTCTGAGATCTAGTGGCTT 1038
 Kv 664 CTTCTGGGTTGGCCATTAGTTCTAGTCTAGTGTACTATTCATATTGATA 723
 Db 1039 CTTCTGGGTTGGCCATTAGTTCTAGTCTAGTGTACTATTCATATTGATA 723
 Kv 1098 CTTCTGGGTTGGCCATTAGTTCTAGTCTAGTGTACTATTCATATTGATA 98
 Db 1159 CACGGCGATCTCCAGCACCACTCTCCATGTTCCAGCTCCAGCAACCAA 1218
 Kv 1099 CGGTTTCAAAACCACTGAGGGCACAGAGAACCTCACTCTGTAATAACATGGAGTAGC 783
 Db 1158 784 CACGGCGATCTCCAGCACCACTCTCCATGTTCTAGCTTGTCCCTCTTAGTTC 903
 Kv 1219 TAGCGCTGTAGTGTAGCATCTGCGCTCTAGCTTGTCCCTCTTAGTTC 903
 Db 1278 TAGCGCTGTAGTGTAGCATCTGCGCTCTAGCTTGTCCCTCTTAGTTC 1278
 Kv 844 TTAATCAGATACTGCTGGAGGCTTCTTACACGCCCTAACAGCAGCTCTTG 963
 Db 1279 TTAATCAGATACTGCTGGAGGCTTCTTACACGCCCTAACAGCAGCTCTTG 1318
 Kv 964 CTAGTGAATTATGCTGGTTTCGTTATGCAAATAATTAAAATG 1020
 Db 1339 CTAGTGAATTATGCTGGTTTCGGTATAGCAAATAATTAAAATG 1395
 Kv
 RESULT 6
 ADY16296
 ID ADY16296 Standard; DNA; 1530 BP.
 XX
 AC ADY16296;
 XX
 DT 05-MAY-2005 (First entry)
 XX
 DR DNA encoding a PRO polypeptide, SEQ ID NO 2102.
 XX
 KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antirheumatic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;

KW
 Kv
 OS Homo sapiens.
 PN WO200516962-A2.
 PD 24-FEB-2005.
 XX
 PF 11-AUG-2004; 2004WO-US026249.
 XX
 PR 11-AUG-2003; 2003US-0493546P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
 DR
 XX
 PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
 XX
 PS Claim 1; SEQ ID NO 2102; 158pp; English.
 XX
 Sequence 1530 BP; 435 A; 361 C; 322 G; 412 T; 0 U; 0 Other;
 SQ
 Query Match 95.8%; Score 984; DB 14; Length 1530;
 Best Local Similarity 98.0%; Pred. No. 2.1e-277;
 Matches 986; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 574
 Db 515 GGGAAATTATAAGAACCTCTTGGCAGTGAACACAGCTGTCACAGATAACA
 Kv 72 TGATCGAAGTGGTCCCCAACGCCACTTTCTCTTCAATTGCGAACAGCT
 Db 575 TGATCGAAGTGGTCCCCAACGCCACTTTCTCTTCAATTGCGAACAGCT
 Kv 132 CCAGAAGGTGGACATACCTTGTCTCTTGTGAAATTTCCTGTGTTTAAGT
 Db 635 CCAGAAGGTGGACATACCTTGTCTCTTGTGAAATTTCCTGTGTTTAAGT
 Kv 191 132 ACATGGCGAAGAGAGAGAACACGTTCTGGATCCAGGGGAAACCCATRA
 Db 695 ACATGGCGAAGAGAGAGAACACGTTCTGGATCCAGGGGAAACCCATRA
 Kv 754 695 ACATGGCGAAGAGAGAGAACACGTTCTGGATCCAGGGGAAACCCATRA
 Db 694 694
 Kv 192 ACATGGCGAAGAGAGAGAACACGTTCTGGATCCAGGGGAAACCCATRA
 Db 755 GACTTACGACACATACATGAAATTAGCTGGTAAAGCTGGCCAGAACGACTGGACAA
 Kv 814 755 GACTTACGACACATACATGAAATTAGCTGGTAAAGCTGGCCAGAACGACTGGACAA
 Db 312 AGAACACAGATGTGAGATGAGATGAAATTAGCTGGTAAAGCTGGCCAGAACGACTGGACAA
 Kv 312 AGAACACAGATGTGAGATGAGATGAAATTAGCTGGTAAAGCTGGCCAGAACGACTGGACAA
 Db 815 AGAACACAGATGTGAGATGAGATGAAATTAGCTGGTAAAGCTGGCCAGAACGACTGGACAA
 Kv 815 AGAACACAGATGTGAGATGAGATGAAATTAGCTGGTAAAGCTGGCCAGAACGACTGGACAA
 Db 372 CTTCTCTCCATAAAGAGGGATCTACATGATCCAAAGAACACATGTCAGA
 Kv 372 CTTCTCTCCATAAAGAGGGATCTACATGATCCAAAGAACACATGTCAGA
 Db 875 CTTCTCTCCATAAAGAGGGATCTACATGATCCAAAGAACACATGTCAGA
 Kv 875 CTTCTCTCCATAAAGAGGGATCTACATGATCCAAAGAACACATGTCAGA
 Db 432 TGCAGATGAACTACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG
 Kv 432 TGCAGATGAACTACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG
 Db 935 TGCAGATGAACTACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG
 Kv 935 TGCAGATGAACTACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG
 Db 492 CCTGCTCTCAAGAGTGTGCTCTTGGCATCATCTGCTGCTGCTGCTG
 Kv 492 CCTGCTCTCAAGAGTGTGCTCTTGGCATCATCTGCTGCTGCTGCTG
 Db 995 CCTGCTCTCAAGAGTGTGCTCTTGGCATCATCTGCTGCTGCTGCTG
 Kv 995 CCTGCTCTCAAGAGTGTGCTCTTGGCATCATCTGCTGCTGCTGCTG 1054

CC is a coronary artery endothelium, umbilical artery or vein endothelium.
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
 CC endothelial, myometrium, dermal microvascular endothelium, keratinocyte
 CC epithelium, bronchial epithelium, mammary epithelium, prostate
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
 CC small airway epithelium, renal epithelium, umbilical artery smooth
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
 CC osteoblasts or prostate stromal cell. The gene expression profile is used
 CC for determining the level of RNA expression for a sample, determining the
 CC phenotype of a cell and distinguishing cell types. The gene or a protein
 CC expression profile is useful in identifying disease pathologies involving
 CC alterations of gene expression. The assessment of expression profiles may
 CC provide meaningful information with respect to tumour type and stage,
 CC treatment methods, and prognosis. The gene or protein expression profile
 CC may also be used for creating microarrays. The microarray is useful for
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue
 CC identifications and in identifying promising antibiotics, antiviral or
 CC antifungal agents

SQ Sequence 1799 BP; 499 A; 434 C; 396 G; 470 T; 0 U; 0 Other;

Query Match 94.3%; Score 968.2; DB 6; Length 1799;
 Best Local Similarity 98.1%; Pred. No. 9; 7e-273; Matches 990; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Matches 990; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Query 20 AAATCANGGTTATGGCCCGGAGAACAGCTATCATTTACAGTAAACACTGTGTCAGATATAACACTGTGAG 79
 Db 791 ATAGAAGACTCTTGGCAGTGACAAACTGTGTCAGATATAACACTGTGAG 850

Query 80 ATGTTCCCAAGGCCCTATTTCTCCCTAATGCTGTAACAAAGCTCCAGAGG 139
 Db 851 ATGTTCCCAAGGCCCTATTTCTCCCTAATGCTGTAACAAAGCTCCAGAGG 910

Query 140 CTGGAACTTACCTTGTGTTCTGAGAATTTCCTGTGATGTTAGAATACATGGC 199
 Db 911 CTGGAACTTACCTTGTGTTCTGAGAATTTCCTGTGATGTTAGAATACATGGC 970

Query 200 AACAAAGAACGAAACAGATCT-GGAGATCCAGGGGAAACACATGAGACTAC 258
 Db 971 AACAAAGAACGAAACAGATCT-GGAGATCCAGGGGAAACACATGAGACTAC 1030

Query 259 GACACATCATGAATTAGCGTAAAGGTGCCAGAACAGACTGACAAAGAAC 318
 Db 1031 GACACATCATGAATTAGCGTAAAGGTGCCAGAACAGACTGACAAAGAAC 1090

Query 319 AGATGATATGTCAGACATGAGAATAATAAACGGAGTTGATCAGAATACTTCT 378
 Db 1091 AGATGATATGTCAGACATGAGAATAATAAACGGAGTTGATCAGAATACTTCT 1150

Query 379 CCATAAAGACGATGTCATCACAAATGATCCAACAGCAATGTTCAAAGATGCAAT 438
 Db 1151 CCATAAAGACGATGTCATCACAAATGATCCAACAGCAATGTTCAAAGATGCAAT 1210

Query 439 GATACACTACTGCTGCACCTCACAAACGCCCTGCAATTACATGTTCTCTGTC 498
 Db 1211 GATACACTACTGCTGCACCTCACAAACGCCCTGCAATTACATGTTCTCTGTC 1270

Query 499 CTCAAGAGCTGGCTATTTGCCATCATCACCTGCTGCTGCTTAGAGAACGGCTTC 558
 Db 1271 CTCAAGAGCTGGCTATTTGCCATCATCACCTGCTGCTGCTTAGAGAACGGCTTC 1330

Query 559 TGCITGCAATGGAGAAGATCATACAGAGGGCATCTTTCATCAAGAGGCCATCTTCTCTC 618
 Db 1331 TGCITGCAATGGAGAAGATCATACAGAGGGCATCTTTCATCAAGAGGCCATCTTCTCTC 1390

Query 619 GGTTATTGCTCTAGAGCGCTGCTCTAGGGACTAGTGGCTTCTCTGGGG 678
 Db 1391 GGTTATTGCTCTAGAGCGCTGCTCTAGGGACTAGTGGCTTCTCTGGGG 1450

RESULT 7

ID AB235381 Standard; cDNA; 1799 BP.

AC AB235381;

XX

DT 05-FEB-2003 (first entry)

DE Human gene expression profile polynucleotide SEQ ID NO 492.

XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
 XX bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
 XX tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
 XX gene expression; gene; ss. Homo sapiens.

XX WO200274979-A2.

XX PD 26-SEP-2002.

XX PF 20-MAR-2002; 2002WO-US008456.

XX PR 20-MAR-2001; 2001US-0276947P.

XX PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX PI Wan J, Wang Y;

XX DR WPI: 2002-740862/80.

XX PT New gene expression profile generated from primary; endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.

XX PS Example 3; Page 634-635; 850pp; English.

XX CC The invention relates to a gene expression profile comprising one or more genes (AB234889-AB235692) and generated from a cell type. The cell type

Best local similarity 97.8%; Pred. No. 3_68-265; Matches 1001; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY	679	CCATTTCAGTTCTCATGTTGTTACTATCTCATATGTTAACGGTTCAACCG	738
Db	1451	CAATTTCAGTTCTCATGTTGTTACTATCTCATATGTTAACGGTTCAACCG	1510
QY	739	TGGGCACACIGAGAACCTCTCTGTAAATACAACTGAGGATAACGGCTTCCAG	798
Db	1511	TGGGCACACAGAGAACCTCTGTAAATACAACTGAGGATAACGGCTTCCAG	1570
QY	799	CAACATCTCCATGTTTCAAGGCTTCCAGGAAACCAAATAGGCCCTGATAG	858
Db	1571	CAACATCTCCATGTTTCAAGGCTTCCAGGAAACCAAATAGGCCCTGATAG	1630
QY	859	TGTAGACATCTGCGCTCTAGCTTGCGCTCTAGTGTCTTAACTACAAT	918
Db	1631	TGTAGACATCTGCGCTCTAGCTTGCGCTCTAGTGTCTTAACTACAAT	1690
QY	919	GCCTGGAAGCTTCAATTTCACGCCCTGAAAGCAGCTTCTTGTAGTGAATTAT	978
Db	1691	GCCTGGAAGCTTCAATTTCACGCCCTGAAAGCAGCTTCTTGTAGTGAATTAT	1750
QY	979	GTTGTTTCCGATAAGCAAAATAATTAAAAAATGAAGT 1027	
Db	1751	GTTGTTTCCGATAAGCAAAATAATTAAAAAATGAAGT 1799	

RESULT 8

AAD38828	ID	AAD38828 standard; cdna; 1418 BP.	
XX	XX		
AC	AC	AAD38828;	
XX	XX		
DT	23-SEP-2002	{ first entry}	
XX	XX		
DE	Human	PSNA cDNA #8.	
XX	XX		
KW	Human; prostate specific protein; PSP; prostate specific nucleic acid; vaccine; transgenic; prostate cancer; gene therapy; transgenic animal; PSNA; 88.		
XX	XX		
OS	Homo sapiens.		
PN	WO200224718-A1.		
XX	XX		
PD	28-MAR-2002.		
XX	XX		
PF	19-SEP-2001; 2001WO-US029386.		
XX	XX		
PR	19-SEP-2000; 2000US-0233746P.		
XX	XX		
PA	(DIAd-) DIADRUX INC.		
XX	XX		
PT	Sun Y, Recipon H, Cafferkey R, Ali S;		
XX	XX		
DR	WPI; 2002-471216/50.		
XX	XX		
PT	Novel isolated prostate specific polypeptide useful for identifying, diagnosing, monitoring, staging, imaging, and treating prostate cancer and non-cancerous disease states in prostate.		
XX	XX		
PS	Claim 1; Page 187; 210pp; English.		
XX	XX		
CC	The invention relates to prostate specific proteins (PSP) and prostate specific nucleic acids (PSNA). Sequences of the invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate. They are also useful for producing engineered prostate tissue for treatment and research. The PSNA sequences are used in gene therapy and for producing transgenic animals and cells. The invention is also used as vaccines. The present sequence is human PSNA cDNA		
CC	Sequence 1418 BP; 418 A; 335 C; 285 G; 380 T; 0 U; 0 Other;		
CC	Query Match	92.1%; Score 945.6; DB 6; Length 1418;	

Best local similarity 97.8%; Pred. No. 3_68-265; Matches 1001; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY	64	CAAGGTGGCAAAATACTGAGTTGGTCCCGAACAAAGCTTCAATTAGAT	63
Db	379	CAAGGTGGCAAAATACTGAGTTGGTCCCGAACAAAGCTTCAATTAGAT	438
QY	439	AAACTCTGATGCGAGAATTCCCAGCCACTATTTCTCTCAATGCTGA	498
Db	124	ACAAGCTCCAGAAGGCTGAACTACCTTGTCTTGAGAAATTTCCTGAT	183
QY	499	ACAAGCTCCAGAAGGCTGAACTACCTTGTCTTGAGAAATTTCCTGAT	558
Db	184	ATTAGATACATTGGCAAGAAGAAGGAAACGATGTTCTGAGAATTTCCTGAT	243
QY	559	ATTAGATACATTGGCAAGAAGAAGGAAACGATGTTCTGAGAATTTCCTGAT	618
Db	244	ACCATGAGACTAACGACACATCATGAATTAGTGTGTTAACGGTCCAGAAAGCTA	303
QY	619	ACCATGAGACTAACGACACATCATGAATTAGTGTGTTAACGGTCCAGAAAGCTA	678
Db	304	CTGACAAAGAACAGATGTTGTCAGATGAGATAATAAACGGAGTGTAA	363
Db	679	CTGGACAAAGAACAGATGTTGTCAGATGAGATAATAAACGGAGTGTAA	738
QY	364	GAATTATCTCCCTCAAATAAAGCAGGATGTCATCACATGGATCCAAAGAACATTG	423
Db	739	GAATTATCTCCCTCAAATAAAGCAGGATGTCATCACATGGATCCAAAGAACATTG	798
QY	424	TCAAAAGATGCAATGATACACTGTGCACTGCAAAACCTCTGCATATTAC	483
Db	799	TCAAAAGATGCAATGATACACTGTGCACTGCAAAACCTCTGCATATTAC	858
QY	484	TACCTCCCTGCTCTAGAGTGTGCTTGTGATGTTGCAATCATACAGAGGTTCTGCTGTT	543
Db	859	TACCTCCCTGCTCTAGAGTGTGCTTGTGATGTTGCAATCATACAGAGGTTCTGCTGTT	918
QY	544	AGAAGAACGCTTCTGCTGAATOGAGAGAAATCATACAGAGGTTCTGCTGCTGTT	603
Db	919	AGAAGAACGCTTCTGCTGAATOGAGAGAAATCATACAGAGGTTCTGCTGCTGTT	978
QY	604	CATCTTCTC-ATCGTATTGCTCTAGAAGGCTCTGAGGAGTAGTGGCT	662
Db	979	CATCTTCTC-ATCGTATTGCTCTAGAAGGCTCTGAGGAGTAGTGGCT	1038
QY	663	TCTTCTGGTTGGCATTCAGTTGCTCATGTTGCTTGTGACTATT-CTATCATATTGTA	720
Db	1039	TCTTCTGGTTGGCATTCAGTTGCTCATGTTGCTTGTGACTATTGTA	1098
QY	721	TAACGTTCAACCAAGTGGCACACAGAGAACCTCTACTCTGTAATACAACTGGAAT	780
Db	1099	TAACGTTCAACCAAGTGGCACACAGAGAACCTCTACTCTGTAATACAACTGGAAT	1159
QY	781	AGCCACGGGATCTCCAGAACCTCTCCATGTTCAACGCTCTCCASCCAAAC	840
Db	1159	AGCCACGGGATCTCCAGAACCTCTCCATGTTCAACGCTCTCCASCCAAAC	1218
QY	841	AATGGCTCTAGTGATGACATCTGGCTTCTGCTCTCTTGTG	900
Db	1219	AATGGCTCTAGTGATGACATCTGGCTTCTGCTCTCTTGTG	1277
QY	901	TCTTATGATGATGCTGGTCTGGTCAATTACGCCCTGAGAGCTCT	960
Db	1278	TCTTATGATGATGCTGGTCTGGTCAATTACGCCCTGAGAGCTCT	1337
QY	961	TTCTAGTGAATTGCTGGTCTGGTCAATTACGCCCTGAGAGCTCT	1020
Db	1338	CTGCTAGTGAATTGCTGGTCTGGTCAATTACGCCCTGAGAGCTCT	1397
QY	1021	AAA 1024	

		RESULT 9
ADB08798/c	ID ADB08798	XX
ADB08798	standard; DNA; 2658 BP.	AC
XX	AC	AC
XX	AC	AC
DT 29-JAN-2004	(first entry)	XX
DE Novel DNA-related contig nucleotide sequence #42.	XX	XX
KW novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; contig; db.	XX	XX
OS Unidentified.	OS	OS
PN WO2003054152-A2.	XX	XX
PD 03-JUL-2003.	XX	XX
PF 10-DEC-2002; 2002W0-US039555.	XX	XX
PR 10-DEC-2001; 2001US-0339739P.	PR	PR
PR 11-DEC-2001; 2001US-0339453P.	PR	PR
PR 14-MAR-2002; 2002US-0365384P.	PR	PR
PR 12-APR-2002; 2002US-0372381P.	PR	PR
PR 22-APR-2002; 2002US-0312855P.	PR	PR
PR 24-APR-2002; 2002US-0376045P.	PR	PR
PA HYSEQ INC.	XX	XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J, Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Dumanac RT, Wang Z; PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ; DR WPI; 2003-569235/53.	XX	XX
PT New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.	XX	XX
PT Disclosure; SEQ ID NO 1864; 1177PP; English.	XX	XX
CC The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence was used in the exemplification of the invention.	CC	CC
CC	CC	CC
XX Sequence 2658 BP; 745 A; 585 C; 578 G; 750 T; 0 U; 0 Other;	SQ	XX
Query Match 89.1%; Score 915; DB 10; Length 2658; Best Local Similarity 97.5%; Pred. No. 4.5e-257; Matches 927; Conservative 0; Mismatches 24; Indels 0; Gaps 0;	Qy	Qy
59 CAGATAAACACTGATCGAGTTCCCAAGCCACTATTTCCTCCTCAATG 118	Qy	Qy
2396 CTGATAAACACTGATCGAGATGTTCCCAAGCCACTATTTCCTCCTCAATG 2337	Db	Db
119 CTGAAACAAGCTCGAGAAGGCTGGACACTTGTCTCTTGAGAAATTTCCTG 178	Qy	Qy
2336 CTGAAACAAGCTCGAGAAGGCTGGACACTTGTCTCTTGAGAAATTTCCTG 2277	Db	Db
179 ATGTTATTAGATCATTCATGGCAAGAACAGAACAGATCTTG3ATCCCAGGG 238	Qy	Qy
2276 ATGTTATTAGATCATTCATGGCAAGAACAGAACAGATCTTG3ATCCCAGGG 2217	Db	Db
RESULT 9		
Qy 239 GGAACACCATGAGACTAACGACACATACATGAAATTAGCTGGTAACGGGCCAGAA 298	Qy	Qy
Db 2216 GGAAACACCATGAGACTAACGACACATACATGAAATTAGCTGGTAACGGGCCAGAG 2157	Db	Db
Qy 299 AGTCACTGGAAAGAACAGAGATGATGCTGAGATGAGATAATAAACGGAGTG 358	Qy	Qy
Db 2156 AGTCATCTGAGAAAGAACAGAGATGCTGAGATAATAAACGGAGTG 2097	Db	Db
Qy 359 ATCAGAAATTATCCTCCCTAAAGAGGATGCTACATGAGATAATAAACGGAGTG 418	Qy	Qy
Db 2096 ATCAGAAATTATCCTCCCTAAAGAGGATGCTACATGAGATAATAAACGGAGTG 2037	Db	Db
Qy 419 TTGTTCAAAGAGCAATGATCACTACTGCTGAGCTACACCTGATTT 478	Qy	Qy
Db 2036 ATTGSGTCAAAGAGCAATGATCACTACTGCTGAGCTACACACCTGTCAT 1977	Db	Db
Qy 479 ACATGTTACCTCTCTGCTCAGAGTGTGCTATTTGCCATCATCACCTCTGTC 538	Qy	Qy
Db 1976 ACATGTTACCTCTCTGCTCAGAGTGTGCTATTTGCCATCATCACCTCTGTC 1917	Db	Db
Qy 539 TGCTTAGAGAAACGSGCTTCTGCTGCAATGGAGAAATCATACAGAGGGGCAAG 598	Qy	Qy
Db 1916 TGCTTGAGAACGSGCTTCTGCTGCAATGGAGAAATCATACAGACGGGCAAG 1857	Db	Db
Qy 599 GAGGGCATCTTCCTGCTCAGGTTATGCTCTATTGCTGAGGCTCTTGAGATCTG 658	Qy	Qy
Db 1856 GAGGCATCTTCCTGCTCAGGTTATGCTCTATTGCTGAGGAGCTCTTGAGATCTG 1797	Db	Db
Qy 659 GCTTCTCTCTGGGTTGGGCAATTCAGCTTCTGAGCTTCTGAGCTTCTGAGATCTG 718	Qy	Qy
Db 1796 GCTTCTCTCTGGGTTGGGCAATTCAGCTTCTGAGCTTCTGAGCTTCTGAGATCTG 1737	Db	Db
Qy 719 TATAGCGTTCAACCCTGGCACAGAACCTGACTCTGAAATACATGAGGA 778	Qy	Qy
Db 1736 TATAATGGTTCTAACACCAGTGGCACAGAACCTGACTCTGAAATACATGAGGA 1677	Db	Db
Qy 779 ATAGCACCGGAGTCCAGACCAATCTCCAGTTTCAAGCTTCAAGCTTCCAGCAC 838	Qy	Qy
Db 1676 ATAGCACCGGAGTCCAGACCAATCTCCAGTTTCAAGCTTCCAGCAC 1617	Db	Db
Qy 839 CAAATAGGGCTCTATAGTTGAGACATCCTGGGGCTCTAGCTTGTCTCTCTGG 898	Qy	Qy
Db 1616 CAAATAGGGCTCTATAGTTGAGACATCCTGGGGCTCTAGCTTGTCTCTCTGG 1557	Db	Db
Qy 899 TGTCTTAACTGATAACTGGCTGGAGGCTTCATTTACACCCCTGAGGCTT 958	Qy	Qy
Db 1556 TGTCTTAACTGATAACTGGCTGGAGGCTTCATTTACACCCCTGAGGCTT 1497	Db	Db
Qy 959 CTGGCTGAGTTATGCTGCTGGCTGGAGGCTT 1009	Qy	Qy
Db 1496 CTGGCTGAGTTATGCTGCTGGAGGCTT 1446	Db	Db
RESULT 10		
ID AAF15623	XX	XX
XX AAF15623 standard; cDNA; 1155 BP.	AC	AC
XX AAF15623;	XX	XX
DT 13-MAR-2001 (first entry)	XX	XX
XX Human prostate cancer antigen nucleotide sequence SEQ ID NO:58.	DE	DE
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerability; gastrointestinal; nephrotropic; antinefective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.	KW	KW
OS Homo sapiens.	OS	OS

PN WO20055174-A1.
 XX
 PD 21-SEP-2000.
 XX
 PR 08-MAR-2000; 2000WO-US005988.
 XX
 PR 12-MAR-1999; 99US-012470P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Ruben SM,
 XX
 DR MPI; 2000-587513/55.
 DR P-PSDB; RAB56420.
 XX
 PT Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer.
 XX
 PS Claim 1; Page 655-656; 2338pp; English.
 CC AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB563 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscle, pulmonary, gastrointestinal, nephrotoxic, antiinfective, gynaecological, and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polypeptides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB7303 represent sequences used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 1155 BP; 359 A; 242 C; 225 G; 317 T; 0 U; 12 Other;
 Query Match 88.2%; Score 906; DB 3; Length 1155;
 Best Local Similarity 97.8%; Pred. No. 1; e-254;
 Matches 951; Conservative 8; Mismatches 8; Indels 5; Gaps 4;
 Qy 59 CAGATAAACACTGTGAGATGTTCCCAAACCCACTATTTCCTCTCAATG 118
 Db 160 CTGATAAACACTGTGAGATGTTCCCAAACCCACTA-TTTCTCTCCTATG 218
 Qy 119 CTGAAACAAAGCTCCAGAAGGGACATACCTTGTCTCTGAGAATTTCCTG 178
 Db 219 CTGAAACAAARCTCGAGAACATACCTTGTCTCTGAGAATTTCCTG 278
 Qy 179 ATGTTATTAACTACATGGCGAGAGAGAGAGAGAACAGATCTGGATCCAGGAG 238
 Db 279 ATTTTATTAACTACATGGCGAGAGAGAGAGAACAGATCTGGATCCAGGAG 338
 Qy 239 CG--AACACCTGAGACTAACATGAAATTAGCGCGTTAACGGGCCAGA 296
 Db 339 CGGACACCATGGAAGACTAACAGAACATACATGAAATTAGCGTTAACGGGCCAGA 398
 Qy 297 AAAGTOACTGGCAAGAACAGAGATGTGT-GAGACATGAG-AATAATAAACGGA 354
 Db 399 AAAGTCACGGAAATTCTTCTCCAAATAAGCGGATTCATCACATGATGCCAA 458
 Qy 355 GTTGATCAAGAAATTCTTCTCCAAATAAGCGGATTCATCACATGATGCCAA 414
 Db 459 GTTGATCAAGAAATTCTTCTCCAAATAAGCGGATTCATCACATGATGCCAA 518
 Qy 415 GACAATGTTCAAGATGCAATGATACACTCTGCGACTCACAAACCTGCA 474
 Db 519 GACAATGTTCAAGATGCAATGATACACTCTGCGACTCACAAACCTGCA 578
 Qy 475 TATACATGAACTCTCTCTCTCAAGGGTGGCTATTGCAATCATCACCTGC 534
 XX
 Query Match 88.2%; Score 906; DB 3; Length 1155;
 Best Local Similarity 97.8%; Pred. No. 1; e-254;
 Matches 951; Conservative 8; Mismatches 8; Indels 5; Gaps 4;
 Qy 59 CAAACCAATAAGGCCCTGATAGTGTGACATCTGGGCTCTAGCTTGCCCTC 894
 Db 835 CAACCCAAATAGGCCCTGATAGTGTGACATCTGGGCTCTAGCTTGCCCTC 894
 Qy 93.9 CAACCCAAATAGGCCCTGATAGTGTGACATCTGGGCTCTAGCTTGCCCTC 998
 Db 895 TAGTGTCTTTAACGATAACTGCCTGAGGCTTCATTACGCCCTGAGAG 954
 Qy 999 TTAGTGTCTTAATCAGATAACTGCCTGAGAACCTTCATTACGCCCTGAGAG 1058
 Qy 955 TCTCTCTCTGTGATGATTGTTGTTTCCCTAATAGCAAAATAATTAA 1014
 Db 1059 TCTCTCTCTGTGATGATTGTTGTTTCCCTAATAGCAAAATAATTAA 1118
 Qy 1015 AAAATGAAAGT 1026
 Db 1119 AAAATGAAARW 1130
 XX
 RESULT 11
 AD0E6987 ID AD0E6987 Standard; DNA; 1560 BP.
 XX
 AC ADE06987;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel coding sequence (useful for identifying genetic disorders) #53.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; gene; ds.
 XX
 OS unidentified.
 XX
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PR 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339439P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSB-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J,
 PI Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Drmanac RT, Wang Z;

PT	Ma Y, Wang D, Chen R, Xu C, Boyle BJ;	QY	674 TTTGGGCCATTTCAGTCATGTGTAATCTATATGTTAACCGTTTCCA 733
DR	WPI; 2003-569235/53.	DB	1207 TTGGGCCATTTCAGTCATGTGTAATCTATATGTTAACCGTTTCCA 1266
DR	P-PSDB; ADE07898.	QY	734 ACCAGTGGCACACAGGAACCTCACTCTGATAACATGAGGATAGCCACGGCATC 793
PT	New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.	DB	1267 ACCAGTGGCACACAGGAACCTCACTCTGATAATGAGGATAGCCACGGCATC 1326
XX	Claim 1; SEQ ID NO 53; 117pp; English.	QY	794 TCCAGCACCAATCTCCAGTTCCAGCTCCAGCTCCAGCACCCAAATAGCCCTGC 853
CC	The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the invention.	DB	1327 TCCAGCACCAATCTCCAGTTCCAGCTCCAGCTCCAGCACCCAAATAGCCCTGC 1386
CC	Sequence 1560 BP; 44 A; 363 C; 322 G; 431 T; 0 U; 0 Other;	QY	854 TATAGTGAGACATCCCTGGCTCTAGCTCTTATCGA 913
CC	Best Local Similarity 91.9%; Score 905.6; DB 10; Length 1560; Matches 987; Conservative 0; Mismatches 39; Indels 48; Gaps 1;	DB	1387 TATAGTGAGACAGCCCTCGGGCTCTAGCTCTTATCGA 1446
QY	2 GGCAAGAGTGCGAAAAAAATCAAGGATTGTCGGAAAGCTTACATTACAG 61	QY	914 TAATGCTGGAGCCCTTCATTTACAGCCCTGAGACAGCTCTTGCTAGTCA 973
Db	487 GAGCAGATAGGATCTTATTAGAACACTTCTGGAGACACACTGTGTCACAG 546	DB	1447 TAATGCTGGAGCCCTTCATTTACAGCCCTGAGACAGCTCTTGCTAGTCA 1506
QY	62 ATAAACAACTTGTGAGATGTTCCCGAACGCCCACATTTCCTCTCAATGCTG 121	QY	974 TATGCTGGTGTTCGGTAAAGCAAATAATTAAAATAGCAAATT 1027
Db	547 ATAAACAACTTGTGAGATGTTCCCGAACGCCCACATTTCCTCTCAATGCTG 606	DB	1507 TATGCTGGTGTTCGGTAAAGCAAATAATTAAAATAGCAAATT 1560
QY	122 AACAGAACGCTCCAGAAGGTGGAACATACCTTCTCTCTGAGAAATTTCCTG 181	RESULT 12	
Db	607 AACAGAACGCTCCAGAAGGTGGAACATACCTTCTCTCTGAGAAATTTCCTG 666	ABL65007	
QY	182 TATTAAGATACATGGCAGAAGAACAGAACACATTCTGGATCCUGGAGGGA 241	ID	ABL65007 standard; DNA; 1421 BP.
Db	667 TATTAAGATACATGGCAGAAGAACAGAACACAGATTCCUGGAGGGA 26	XK	
QY	242 ACACCATGAGCTAACGACATACATGAAATTAGCTGGTAAACGGTCCGAAAGT 301	AC	
Db	727 ACACCATGAGCTAACGACATACATGAAATTAGCTGGTAAACGGTCCGAAAGT 786	XX	
QY	302 CACTGGACAAAGAACAGATGTATGTCAGACATGAGAAATTAAACGGATGTC 361	DT	15-MAY-2002 (first entry)
Db	787 CACTGGACAAAGAACAGATGTATGTCAGACATGAGAAATTAAACGGATGTC 846	XX	
QY	362 AGAAATTATCTTCTCCAAATAAGAC-----	DE	
Db	847 AGAAATTATCTTCTCCAAATAAGACAGATGTACCAACAGTGGATCCAAAGACATT 906	XX	
QY	390 -----GGATGCTCAGATGGATCCAAAGACAACTGTTCAAAGATG 433	XK	
Db	907 ATTCAAAAGATGCAATGATGTCACTACAGATGATCCAAAGACAATGGTAAAGATG 966	PN	
QY	434 CAATGATACATACTGTGCGAGCTCACAAACACCTCTGCAATTACATGTCCTCC 493	XX	
Db	967 CAATGATACATACTGTGCGAGCTCACAAACACCTCTGCAATTACATGTCCTCC 1026	PD	13-DEC-2001.
QY	554 CTTCCTGCTCAACTGAGAACATCAACAGACGGTCCACAGGGCCCTTTC 613	XX	
QY	494 TGCCTCTGCTCAAGAGTGGCTATTGTCCATCATCACCTGCTCTGCTGTTAAGAACGG 553	PF	30-MAY-2001; 2001WO-US010838.
Db	1087 CTTCCTGCTCAACTGAGAACATCAACAGACGGTCCACAGGGTCCACCTTTC 1146	PR	05-JUN-2000; 2000US-0209473P.
Db	1027 TGCCTCTGCTCAAGAGTGGCTATTGTCCATCATCACCTGCTGCTGTTAAGAACGG 1086	PR	05-JUN-2000; 2000US-0209531P.
QY		PR	18-SEP-2000; 2000US-0233133P.
Db		PR	18-SEP-2000; 2000US-0233617P.
QY		PR	20-SEP-2000; 2000US-0234009P.
Db		PR	20-SEP-2000; 2000US-0234034P.
QY		PR	20-SEP-2000; 2000US-0234022P.
Db		PR	22-SEP-2000; 2000US-023409P.
QY		PR	22-SEP-2000; 2000US-023457P.
Db		PR	25-SEP-2000; 2000US-0234923P.
QY		PR	25-SEP-2000; 2000US-0234924P.
Db		PR	25-SEP-2000; 2000US-023507P.
QY		PR	25-SEP-2000; 2000US-023502P.
Db		PR	27-SEP-2000; 2000US-023520P.
QY		PR	27-SEP-2000; 2000US-023534P.
Db		PR	28-SEP-2000; 2000US-023538P.
QY		PR	28-SEP-2000; 2000US-0236038P.
Db		PR	28-SEP-2000; 2000US-0236033P.

PD	10-SEP-2004.	QY	200 AAGAAAGAGGACACUGATCTGGATCCAGGGAAACCCGTGAAGACTAACG 259
PF	22-FEB-2004; 2004WO-DE000433.	QY	549 AAGGAGAGGAGCAACAGATTCTGGATCCAGGGAAACCCGTGAAGACTAACG 608
XX		Db	549 AAGGAGAGGAGCAACAGATTCTGGATCCAGGGAAACCCGTGAAGACTAACG 608
PR	27-FEB-2003; 2003DE-01009985.	QY	260 ACCATAATGAAATTGGTGTGTTAAGGGTCCAGAAAGTCACSGACAAGACCA 319
PR	14-MAY-2003; 2003DE-01022134.	PA	(HINZ/) HINZMANN B.
XX		PA	(DAHL/) DAHL E.
DR		PA	(ROSE/) ROSENTHAL A.
PA		PA	(HERM/) HERMANN K.
PA		PA	(PLLA/) PILASSKY C.
XX		PA	
PI	Hinzmann B., Dahl E., Rosenthal A., Hermann K., Pilarsky C., Specht T;	QY	320 GATGTATGTCAGACATGAGATAAAACCGAGTTGATCAAGAATATCTTC 379
PI	Schmitt A., Beckmann G., Bruemendorf T., Kinnemann H., Roepcke S;	QY	669 GATGTATGTCAGACATGAGATAAAACCGAGTTGATCAAGAATATCTTC 728
XX	Xinzhong L., Staub E;	Db	669 GATGTATGTCAGACATGAGATAAAACCGAGTTGATCAAGAATATCTTC 728
DR		Db	
WPI:	2004-653386/3.	QY	392 ATGTCATACAMTGTGATCCAAGAACAGATAAGATCAAAGATGCAATCTACTGC 451
PT	New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding agents.	Db	789 ATGTCATACAMTGTGATCCAAGAACAGATAAGATCAAAGATGCAATCTACTGC 848
PT		Db	729 CAATRAAGACAGATGTCAACCACAGTGGTCCAAAGAGAGTATTCAAAGATGCAATG 788
PS	Claim 1; Page 282; 1607pp; German.	QY	452 TGCAGCTCAAAACCTCTGATCATGACTCTCTGCTCTGCTCTCAAGAGTGCG 511
XX		Db	849 TGCAGCTCAAAACCTCTGATCATGACTCTCTGCTCTGCTCTCAAGAGTGCG 908
CC	This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention.	QY	512 TCTATTTGCCATCATCCTGCTGCTGCTAGAGAACGGCTTCGCTGCTGATGGG 571
CC		Db	909 TCTATTTGCCATCATCCTGCTGCTGCTAGAGAACGGCTTCGCTGCTGATGGG 968
CC		QY	572 AGAAATCTAACGACAGCTGAGCTGATGACTGCTCTCTGCTCATCGTTATGTCCT 631
CC		Db	969 AGAAATCTAACGACAGCTGAGCTGAGCTGCTCTCTGCTCATCGTTATGTCCT 1028
CC		QY	632 AGAAGGCTTCTGAGGAGCTAGTGCGCTTCTCTGGTTGGCACATTGAGT 691
CC		Db	1089 CATGTGTTACTATCTCATCATPATGTTAATGTTCAACCCAGTGGCACAGAG 1148
CC		QY	1029 AGAGGCTTCTGAGGAGCTACTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1088
CC		Db	752 AACCTCATCTGTAACAACTGAGGATAGCCACGGCATCTCCAGACCAACTCTCC 811
CC		QY	692 CATGTGTTACTATCTCATATTGATAACGGTTCAACCCAGTGGCACAGAG 751
CC		Db	1149 AACCTCATCTGTAACAACTGAGGATAGCCACGGCATCTCCAGACCAACTCTCC 1208
CC		QY	812 ATGTTTACAGCTCCAGCCACCCAAATAGCGCTGCTATAGTTGAGCATCTG 871
CC		Db	1209 ATGTTTACAGCTCCAGCCACCCAAATAGCGCTGCTATAGTTGAGCATCTG 1268
CC		QY	872 CGGCTCTGCGCTCTGCTCTGCTTAGTGTCTTAATCGATAACTCGCTGAGACCTT 931
CC		Db	1269 CGGCTCTGCGCTCTGCTCTGCTTAGTGTCTTAATCGATAACTCGCTGAGACCTT 1328
CC		QY	932 TCATTTACGCGCTGAGGAGCTCTTGTGTTAGTTGAAATTAGTGCTGCTGCTGAGCC 991
CC		Db	1329 TCATTTACGCGCTGAGGAGCTCTTGTGTTAGTTGAAATTAGTGCTGCTGAGCC 1388
XX	Sequence 1421 BP; 419 A; 325 C; 292 G; 385 T; 0 U; 0 Other;	QY	992 GTATAAGCAAAATAATTAAAGAAGAA 1024
QY	Query Match Best local Similarity 87.8%; Score 902.2; DB 13; Length 1421; Matches 977; Conservative 0; Mismatches 28; Indels 48; Gaps 1;	Db	1389 GTATAAGCAAAATAATTAAAGAAGAA 1421
QY		RESULT 14	
Db		ADR66783	
Db		ID ADR66783	standard; DNA; 1421 BP.
QY	80 ATGTTTCCGCCAACCCACTTTCTCTCTCATCTGAGAACAGCTCCAGAAG 139	XX	
Db	429 ATGTTTCCGCCAACCCACTTTCTCTCTCATCTGAGAACAGCTCCAGAAG 488	AC	ADR66783;
QY	140 CTGGACACATACCTGTCTCTGAGAAATTTCCTGATGTTAATAGATCATGCC 199	DT	02-DEC-2004 (first entry)
Db	489 CTGGACACATACCTGTCTCTGAGAAATTTCCTGAGATATTAGATCATGCC 548	XX	Human prostatic carcinoma derived DNA SEQ ID 76 #4.
KW	human; cytostatic; diagnosis; prostatic cancer;		

OS	XX	KW	differential expression analysis; ds.
XX	XX	XX	Home sapiens.
PN	WO2004076614-A2.	QY	
PD	10-SEP-2004.	QY	
PF	22-FEB-2004; 2004WO-DE000433.	QY	
PR	27-FEB-2003; 2003DE-0100985.	Db	
PR	14-MAY-2003; 2003DE-01022134.	Db	
XX	PA (HINZ/)	PA (HINZ/)	HINZMANN B.
PA	(DAHL/)	PA (DAHL/)	DAHL B.
PA	(ROSE/)	PA (ROSE/)	ROSENTHAL A.
PA	(HERM/)	PA (HERM/)	HERMANN K.
PA	(PILA/)	PA (PILA/)	PILARSKY C.
XX	PI	PI	HINZMANN B., Dahl B., Rosenthal A., Hermann K., Pilarsky C., Specht T;
PI	Xinzhang L., Staub E;	DB	
XX	DR	DR	
XX	PT	PT	New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding agents.
PS	WPI: 2004-653386/63.	QY	
XX	Claim 1; Page 1452; 160pp; German.	QY	
CC	This invention describes novel cytoplastic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal); antibody directed against Ab or any of the above derivatives with a reporter group, cell toxin, immunosimulatory molecules and/or radioloscope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD4 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. Ad65805-Ad66954 represent the invention.	QY	
CC	Sequence 1421 BP; 419 A; 325 C; 292 G; 385 T; 0 U; 0 Other;	QY	
CC	Query Match 87.8%; Score 902.2; DB 13; Length 1421; Best Local Similarity 92.8%; Pred. No. 1.9e-253; Mismatches 977; Conservative 0; Mismatches 28; Indels 48; Gaps 1;	Db	
CC	Matches 369 ATAGAAGACTTGTGCAAGAACACAGTCATGTCAGATAACACTGTGAG 428	Db	
CC	CC 80 ATGTTCCCCAACGCCCACTATTTCCTCTCATGGTGAACAAAGCTCCGAAG 139	Db	
SQ	Sequence 1421 BP; 419 A; 325 C; 292 G; 385 T; 0 U; 0 Other;	Db	
QY	RESULT 15	QY	
QY	20 AAATCAGGATTGTCGCCGAAAGCTATCATACAGATAACACTGTGAG 79	ABKG4529	
QY	369 ATAGAAGACTTGTGCAAGAACACAGTCATGTCAGATAACACTGTGAG 428	ID ABKG4529	standard; DNA; 1586 BP.
QY	80 ATGTTCCCCAACGCCCACTATTTCCTCTCATGGTGAACAAAGCTCCGAAG 139	XX	
Db	429 ATGGTTCCCCAACGCCCACTATTTCCTCTCATGGTGAACAAAGCTCCGAAG 498	AC	
QY	140 CTGGACATACACTTGCTCTTGAGAAATTTCCTGATGTTATAGATCACGGC 199	ABKG4529	
Db	489 CTGGACATACACTTGCTCTTGAGAAATTTCCTGATGTTATAGATCACGGC 549	ID ABKG4529	
Db	200 AAGAAAAGAGGCAACAGCGATCTGGATCCAGGAGGGACACCCTGAACTAACG 259	XX	
Db	549 AGAAAGAAGAGGCAACAGCGATCTGGATCCAGGAGGGACACCCTGAACTAACG 608	AC	
Db	260 ACAGATAGTAGTTAGCTGTTAACCGTGCAGAAGACACTGGACAGAACACA 319	ABKG4529	
Db	609 ACAGATAGTAGTTAGCTGTTAACCGTGCAGAAGACACTGGACAGAACACA 668	ID ABKG4529	
Db	320 GATGATGCTGAGCATGAGATAAAACCGAGTGTAGAAGAAATTCTTCCTC 379	XX	
Db	669 GATGATGCTGAGCATGAGATAAAACCGAGTGTAGAAGAAATTCTTCCTC 728	AC	
Db	380 CATTAAGAC-----GG 391	ABKG4529	
Db	729 CAATTAAGACAGTGTACCCAAAGACAGTATGCAAGAGCTGTTCAAAGATGCAAATG 778	ID ABKG4529	
Db	392 ATGTCATCACATGATGATCCAAAGACAATTGTCAAAGATGCAATGATACTACTGC 451	XX	
Db	789 ATGTCATCACATGATGATCCAAAGACAATTGTCAAAGATGCAATGATACTACTGC 648	AC	
Db	452 TGCAGCTCAACACCTCTGCGATATTACATGATGCTCTCTGCTCTGCTCAAGATGTRGG 511	ABKG4529	
Db	849 TGCAGCTCAACACCTCTGCGATATTACATGATGCTCTCTGCTCTGCTCAAGATGTRGG 908	ID ABKG4529	
Db	512 TCTTTTCCATCATCACCTGCGATATTACATGATGCTCTCTGCTCTGCTCAAGATGTRGG 571	XX	
Db	909 CTATTTTCCATCATCACCTGCGATATTACATGATGCTCTCTGCTCTGCTCAAGATGTRGG 968	AC	
Db	572 AGAAATCATAAAGACGGCTGCAAGAGGGCCATCTTTCCTCTCATCGTTATGTCCT 631	ABKG4529	
Db	969 AGAAATCATAAAGACGGCTGCAAGAGGGCCATCTTTCCTCTCATCGTTATGTCCT 1028	ID ABKG4529	
Db	632 AGAAGCGCTTCTGAGGATCTAGTGGCTTCTGCTCTGCTCTGCTCTGCTCAAGATGTRGG 691	XX	
Db	1029 AGAAAGCTCTCTGAGGATCTAGTGGCTTCTGCTCTGCTCTGCTCAAGATGTRGG 1088	AC	
Db	692 CATGGTGACTATCTCATTTGATACGGTTCAACCAAGGGCTTCTGCTCAAGATGTRGG 751	ABKG4529	
Db	1089 CATGGTGACTATCTCATTTGATACGGTTCAACCAAGGGCTTCTGCTCAAGATGTRGG 1148	ID ABKG4529	
Db	752 AACCTCACTCTGTTAAACATGAGGATAGCCACGGCATCTCAGCACCACTCTCC 811	XX	
Db	1149 AACCTCACTCTGTTAAACATGAGGATAGCCACGGCATCTCAGCACCACTCTCC 1208	AC	
Db	812 ATGTTTCCACAGCTCTCCAGCAACCAAATGGCGCTCTAGTGTAGACATCTG 871	ABKG4529	
Db	1209 ATGTTTCCACAGCTCTCCAGCAACCAAATGGCGCTCTAGTGTAGACAGCTG 1268	ID ABKG4529	
Db	872 CGGCTCTGAGCTCTGCTCTCTGCTCTAGTGTAGACATCTG 931	XX	
Db	1269 GGCTCTGAGCTCTGCTCTCTGCTCTAGTGTAGACATCTGCTGGAGCT 128	AC	
Db	932 TCATTTACAGGCCCTGAGGAGCTCTGCTCTAGTGTAGATATGTTGTTTC 991	ABKG4529	
Db	1329 TCATTTACAGGCCCTGAGGAGCTCTGCTCTAGTGTAGATATGTTGTTTC 1388	ID ABKG4529	
Db	992 GTAAATGACAAATAATTAAATGAAA 1024	XX	
Db	1389 GTAAATGACAAATAATTAAATGAAA 1421	AC	

THIS PAGE BLANK (USPTO)

QY	181 GTTAAACATGGAGGAAAGGAAAGGAAACAGATTCTGGATCCCGAGGG 240	REFERENCE 1 (sites)
Db	181 GTTAAACATGGAGGAAAGGAAAGGAAACAGATTCTGGATCCCGAGGG 240	AUTHORS Essand,M., Vasmatzis,G., Brinkmann,U., Duray,P., Lee,B. and Pastan,I.
QY	241 AACACCATGAGACTAACGACACATAGAAATTAGTGTGTACGGTCCAGAAG 300	TITLE High expression of a specific T-cell receptor gamma transcript in epithelial cells of the prostate
Db	241 AACACCATGAGACTAACGACACATAGAAATTAGTGTGTACGGTCCAGAAG 300	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (16), 9287-9292 (1999)
QY	301 TCACTGACAGAGAACACAGATGATGTCAGACATGAAATTAGTGTGTACGGTCCAGAAG 360	PUBLMED 10430935 2 (bases 1 to 1027)
Db	301 TCACTGACAGAGAACACAGATGATGTCAGACATGAAATTAGTGTGTACGGTCCAGAAG 360	REFERENCE Wolfgang,C.D., Essand,M., Vincent,J.J., Lee,B. and Pastan,I. TARP: a nuclear protein expressed in prostate and breast cancer cells derived from an alternate reading frame of the T cell receptor gamma chain locus
QY	361 CAAGAATTCTTCTCCATAAGACGGATGTCATGAAATTAGTGTGTACGGTCCAGAAC 420	PROC. NATL. ACAD. SCI. U.S.A. 97 (17), 9437-9442 (2000)
Db	361 CAAGAATTCTTCTCCATAAGACGGATGTCATGAAATTAGTGTGTACGGTCCAGAAC 420	3 (bases 1 to 1027)
QY	421 TGTCTCAAAGTGCAATGATACTACTGCTGCGCTCACAAACCTCTGCATATTAC 480	AUTHORS Essand,M., Vasmatzis,G., Brinkmann,U., Duray,P., Lee,B. and Pastan,I.
Db	421 TGTCTCAAAGTGCAATGATACTACTGCTGCGCTCACAAACCTCTGCATATTAC 480	JOURNAL Direct Submission
QY	481 ATGACTCTCTCTGTCAGAGTGTGCTTGCATACCTGCATCCAGGAGTGTCTG 540	Submitted (13-MAY-1999) Division of Basic Sciences, Laboratory of Molecular Biology, National Institutes of Health, National Cancer Institute, 37 Convent Drive, Bethesda, MD 20892, USA
Db	481 ATGACTCTCTCTGTCAGAGTGTGCTTGCATACCTGCATCCAGGAGTGTCTG 540	LOCATION/QUALIFIERS 1..1027
QY	541 CTTAGAGAAGGGCTTCGTCATGGAGAAATCATACAGACGGTGGCAGAAA 600	FEATURES Source organism="Homo sapiens"
Db	541 CTTAGAGAAGGGCTTCGTCATGGAGAAATCATACAGACGGTGGCAGAAA 600	/mol_type="mRNA" /db_xref="tcxon:9606"
QY	601 GGCATCTTCTCATGGTATGTCCTAGAAGGTGTCCTCTGAGGATCTACTGGC 660	gene note="transcript from an unrearranged TCRG locus" 1..1027
Db	601 GGCATCTTCTCATGGTATGTCCTAGAAGGTGTCCTCTGAGGATCTACTGGC 660	gene="TCRG" 1..60
QY	661 TTCTCTCTGGTTGGCCATTCAGTCATGTCAGTATCTATATTGTA 720	CDS gene="TCRG" note="Gamma 1; corresponds to exon I" 74..250
Db	661 TTCTCTCTGGTTGGCCATTCAGTCATGTCAGTATCTATATTGTA 720	/gene="TCRG" note="Gamma 1; corresponds to exon I" 61..390
QY	721 TAACGTTTAAACAGTGGCACAGAACCTACTCTGTTAAATCATGAGGAAT 780	C_region gene="TCRG" note="TCRG" product="TCRGamma alternate reading frame protein" protein_id="P42933"; start=1
Db	721 TAACGTTTAAACAGTGGCACAGAACCTACTCTGTTAAATCATGAGGAAT 780	/product="TCRGamma alternate reading frame protein" protein_id="P42933"; start=1
QY	781 AGCCAGGGCTGCTCCAGAACATCTCCATGTTTCCACAGCTCTCCAGCAACC 840	/transliteration="MQWRPPSLFFFLQLKQSSRRLHEHTVFLRNFSLMILRYIGKK RRAIRFMDPRRGTP 391..438
Db	781 AGCCAGGGCTGCTCCAGAACATCTCCATGTTTCCACAGCTCTCCAGCAACC 840	gene="TCRG" note="Gamma 1; corresponds to exon II" 429..579
QY	841 AAATAGCGCTCTATAGTGTGAGACATCTCGTGGCTCTGTCCTCTTAGTG 900	gene="TCRG" note="Gamma 1; corresponds to exon III" 901 TTCTTAACTGAGATACTGCCTGGAGACCTCTTCAGCTCTGTCCTCTAGTG 960
Db	841 AAATAGCGCTCTATAGTGTGAGACATCTCGTGGCTCTGTCCTCTAGTG 900	C_region gene="TCRG" note="Gamma 1; corresponds to exon III" 901 TTCTTAACTGAGATACTGCCTGGAGACCTCTTCAGCTCTGTCCTCTAGTG 960
QY	961 TTCTGTTGATTAGTGTGTTTCGTAATAGCAAAATAATTAAATG 1020	ORIGIN Query Match Best Local Similarity 100.0%; Score 1027; DB 8; Length 1027; Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	961 TTCTGTTGATTAGTGTGTTTCGTAATAGCAAAATAATTAAATG 1020	QY 1 GGGCAAGAGTTGGCAAAATCAAGGTTGTCCTGCGGAACAAGCTATCATACA 60
QY	1021 AAAAGTT 1027	Db 1 GGGCAAGAGTTGGCAAAATCAAGGTTGTCCTGCGGAACAAGCTATCATACA 60
Db	1021 AAAAGTT 1027	QY 61 GATAAACATGGAGGAAATGGTTCCTCCAGCAATTTCCTCTCAATTCT 120
RESULT 2		Db 61 GATAAACATGGAGGAAATGGTTCCTCCAGCAATTTCCTCTCAATTCT 120
AF151103	AF151103 Homo sapiens 1027 bp linear PRI 03-NOV-2000	DEFINITION complete cds.
LOCUS	AF151103 Homo sapiens TCRgamma alternate reading frame protein (TCRG) mRNA, complete cds.	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
	AF151103 GI:5758136	Homo sapiens (human)
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

		REMARK	
Db	601 GGCCATCTTCTCATCGGTTATGCCAGAAGGCTTCCTGGATTCTGTGGC	660 USA	
Qy	661 TTCTTCTTCTGGCTTGGCCATTCTGGTTCTCATGGTGTACTATCTATATGTA	NIH-MGC Project URL: http://mgc.nci.nih.gov	
Db	661 TTCTTCTTCTGGCTTGGCCATTCTGGTTCTCATGGTGTACTATCTATATGTA	Contact: MGC help desk	
Qy	721 TAACGTTTCAACAGTGGCACAGAACCTACTCTGATACTATGAACTATGTA	Email: cgbps@mail.nih.gov	
Db	721 TAACGTTTCAACAGTGGCACAGAACCTACTCTGATACTATGAACTATGTA	Tissue Preparation: Life Technologies, Inc.	
Qy	781 AGCCAGGGGAACTCCAGCACAACTCTCCATGTTCCAAGGCTCTCGGACACC	CDNA Library Preparation: Life Technologies, Inc.	
Db	781 AGCCAGGGGAACTCCAGCACAACTCTCCATGTTCCAAGGCTCTCGGACACC	CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LNU)	
Qy	841 AAATAGGGCTCTATAGTGAGACATCCCTGGGTCTAGCTGTTAAATAGGAA	CDNA Sequencing by: National Institutes of Health Intramural	
Db	841 AAATAGGGCTCTATAGTGAGACATCCCTGGGTCTAGCTGTTAAATAGGAA	Sequencing Center (NISC),	
Qy	841 AAATAGGGCTCTATAGTGAGACATCCCTGGGTCTAGCTGTTAAATAGGAA	Gaithersburg, Maryland;	
Db	901 TCTTTAATCGATAACTGGGAGCCTTCATTACGGCTGAGGAGCTCT	Web site: http://www.nisc.nih.gov	
Qy	901 TCTTTAATCGATAACTGGGAGCCTTCATTACGGCTGAGGAGCTCT	Contact: nisc.mgc@nigri.nih.gov	
Db	901 TTCTTAACTCGATAACTGGGAGCCTTCATTACGGCTGAGGAGCTCT	Akter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,	
Qy	960 961 TTGCTAGTGTGATTATGGGTTTCGTAATAGCAAATAATTAAAATG	Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,	
Db	961 TTGCTAGTGTGATTATGGGTTTCGTAATAGCAAATAATTAAAATG	Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P.,	
Qy	1020 1021 AAGATT 1027	Hansen, N., Ho, S.-L., Karlin, E., Kong, P., Juric, P., Legaspi, R.,	
Db	1021 AAGATT 1027	Maduro, Q.L., Maniello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stanticop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.I., Walker, M.A., Weatherby, K.D., Wiggins, L., Young, A., Zhang, L.H. and Green, E.D.	
REFERENCE	BC072396	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNU site: http://image.lni.nih.gov	
AUTHORS	BC072395	Series: IRAK plate: 174 Row: c Column: 15	
VERSION	BC072396.1	This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.	
SOURCE	MGC.	Location/Qualifiers	
ORGANISM	Homo sapiens	1..1825	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eutheriongilia; Primates; Catarrhini; Hominoidea; Homo;	FEATURES	Source	
1..(bases 1 to 1825)			
Stausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Attachul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heleb, F., Diachenko, L., Marusin, K., Farmer, A.R., Rubin, G.M., Hong, L., Stipleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carinci, P., Prange, C.S., Rana, S.S., Loqueline, N.A., Peters, G.J., Abramson, R.D., Mulahy, S.J., Bosak, S.A., McElwan, P.J., McErnan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalon, D.K., Muniz, D.M., Soderberg, B.J., Lu, X., Gibbs, R.A., Faleh, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madden, A., Young, A.C., Shevchenko, Y., Boutefeld, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grifmon, J., Schmutz, J., Myers, R.M., Butterfield, V.S., Krzywinski, M.I., Skalska, U., Smalius, D.E., Schinnerich, A., Schein, J.E., Jones, S.J. and Marra, M.A.	gene		
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	ORIGIN	
PUBLMED	1247932	Query Match	
REFERENCE	2 (bases 1 to 1825)	Best Local Similarity	99.3%; Score 1010; DB 8; Length 1825;
AUTHORS	Strausberg, R.	Matches	1013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
TITLE	Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer	General	7 GAGTTGGCAGAAATCAGGATTGGCTCCGAACTAACGTTACATGAGATAA 66
JOURNAL		Db	750 GAGTTGGCAGAAATCAGGATTGGCTCCGAACTAACGTTACATGAGATAA 809
		Qy	67 CAACTGAGTGGCAGAAATCAGGATTGGCTCCGAACTAACGTTACATGAGATAA 126
		Db	810 CAACHTGAGTGGCTCCGAACTAACGTTACATGAGATAA 869
		Qy	127 AAGCTTGGAGGGGAGTGGACATCTTGTGCTTGTGAAGATTTCCTGATGTTA 186

	AUTHORS
OY	870 AACCTTCAGAGGCTGGAACATCCCTTCTCTTGTGAATTGTTT 929
OY	187 AACATACATGSCAGAGAAGAACATACATCCCTTCTCTTGTGAATTGTTT 929
OY	247 ATGAGACTAACACAATCATGAAATTAGTGTTAACGGTCCAGAAGTCACTG 306
OY	990 ATCAGAGACTAACATGAAATTAGTGTTAACGGTCCAGAAGTCACTG 1049
Db	930 AACATACATGGGAGAGAAAGAGAACACAGATCTGGATCCAGGGAGACCC 989
OY	307 GACAAGAACACAGATGTATCGTAGACATGAGATAATAAACGGGTTGATCAAGA 366
OY	427 AAGATGCAATGATACACTACTGGCGCTCAAACACTCTGGATATACATGTC 486
OY	1170 AAGATGCAATGATACACTACTGGCGCTCAAACACTCTGGATATACATGTC 1109
Db	367 ATTATCTTCATGAAAGACGGATCATCACGATGATCCAAAGAACATTGTC 426
Db	1110 ATTATCTTCATGAAAGACGGATCATCACGATGATCCAAAGAACATTGTC 1169
OY	487 CTCTCTCTGCTCTCTCAAGAGTGTGCTATTCGATCATCACCTGCTGCTTGA 546
OY	1230 CTCCTCTCTCTCAAGAGTGTGCTATTCGATCATCACCTGCTGCTTGA 1229
OY	547 AGAACGCTTCTGCATGAGGAATCATACAGACGGTGCATCACGATGATCCAAAGGGCAT 606
Db	1290 AGAACGCTTCTGCATGAGGAATCATACAGACGGTGCATCACGATGATCCAAAGGGCAT 1349
OY	607 CTTTCTCATCGGTTATGCTCTATGCTCTGCTATGCTCTGCTATGCTCTGCTT 666
OY	667 TCTGGTTGGCCATTCTGCTCTGCTATGCTCTGCTATGCTCTGCTT 726
Db	1350 CTTTCTCATCGGTTATGCTCTGCTATGCTCTGCTATGCTCTGCTT 1409
OY	1410 TCTGGTTGGCCATTCTGCTCTGCTATGCTCTGCTATGCTCTGCTT 1469
OY	727 TTTCACACGAGTGGCACAGAGAACCTCACTCTGTTAACTGAGGAATGGCAC 786
Db	1470 TTTCACACGAGTGGCACAGAGAACCTCACTCTGTTAACTGAGGAATGGCAC 1529
OY	787 GGGGATCTCAGAACAACTCTCCATGTTCCACAGCTCTCCAGGCCAACCAATAG 846
OY	1530 GGGGATCTCAGAACAACTCTCCATGTTCCACAGCTCTCCAGGCCAACCAATAG 1589
OY	847 CGCTGCTATAGTGAGATCTCGGCTCTAGCTTGCTCTCTTAGTGTTCTT 906
Db	1590 CGCTGCTATAGTGAGATCTCGGCTCTAGCTTGCTCTCTTAGTGTTCTT 1649
OY	907 ATTCAGATRACTGCTGGAGCTTCATTACGGCTGAGAGCTCTCTGCTA 966
Db	1650 AATCGATTAACCTCTGGAGCTCTTACGGCTGAGAGCTCTCTGCTA 1709
OY	967 GTTGATATGGTGTGTTGGTAAAGGAAATAATTAAAGAA 1024
Db	1710 GTGAGATATGGTGTGTTGGTAAAGGAAATAATTAAAGAA 1767
RESULT 5	
LOCUS	BC062761 1054 bp mRNA linear PRI 16-DBC-2003
DEFINITION	Homo sapiens T cell receptor gamma variable 9, mRNA (cDNA clone)
ORGANISM	Homo sapiens (human)
VERSION	BC062761.1 GI:38540986
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;	
Hominidae; Homo; Homo	
REFERENCE	I (bases 1 to 1054)
FEATURES	
source	1. 1..1054
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAG:4248993"
	/tissue_type="Prostate"
	/clone_Tube="NIH_MGC_83"
	/lab_host="DH10B"
	/note="Vector: pDONR-LIB"
	<1..1054
	/gene="TRGV9"
	/note="synonyms: TRGV9, V2"
	/db_xref="GeneID:6983"
	/ab_xref="IMGT/LIGM:TRGV9"
	<1..577
	/gene="TRGV9"
	/codon_start=2
	/product="TRGV9 protein"
	/protein_id="AAH2761.1"
CDS	

ORIGIN

```

Query Match 98.2%; Score 1008.8; DB 8; Length 1054;
Best Local Similarity 99.8%; Pred. No. 1.7e-248;
Matches 1010; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 16 AAAAATACAGGTATTGGTCCGGACAAAGCTATCATACAGATAAACACTGT 75
Db 11 AAAMATACAGGTATTGGTCCGGACAAAGCTATCATACAGATAAACACTGT 70
Qy 76 GCAGATGTTCCCCAGGCCACTATTTCTCAATTGCTGAACAAACCTCCG 135
Db 71 GCAGATGTTCCCCAGGCCACTATTTCTCAATTGCTGAACAAACCTCCG 130
Qy 136 AGGGCTGGAAAGATACTCTTGCTCTTGAGAATTTCCTGATGTATTAGATCAT 195
Db 131 AGGGCTGGAAAGATACTCTTGCTCTTGAGAATTTCCTGATGTATTAGATCAT 190
Qy 196 TGGCAGAAGAAAGAGCAACAGGCTCGGATCCAGGGGAAACACATGAGCT 255
Db 191 TGGCAGAAGAAAGAGCAACAGGCTCGGATCCAGGGGAAACACATGAGCT 250
Qy 256 AACGACACATACATGAAATTAGCTGGTTAACGGTGCAGAAAGTCACTGACAAAGA 315
Db 251 AACGACACATACATGAAATTAGCTGGTTAACGGTGCAGAAAGTCACTGACAAAGA 310
Qy 316 CACAGATGTTGTCAGACATGAGAATAAAACGGACTGATCAAGAATTCTT 375
Db 311 CACAGATGTTGTCAGACATGAGAATAAAACGGACTGATCAAGAATTCTT 370
Qy 376 CCTCCATAAAGACGGATGTCATCAAACTGATCCAAAGAACATGTCAGAATGCA 435
Db 371 CCTCCATAAAGACGGATGTCATCAAACTGATCCAAAGAACATGTCAGAATGCA 430
Qy 436 ATGATACTACTACTGCACTCACAAACCTCTGCAATTATGTAACCTCTG 495
Db 431 ATGATACTACTACTGCACTCACAAACCTCTGCAATTATGTAACCTCTG 490
Qy 496 CTCTCAAGAGGTCTTATTCGTCATCTCAGGAAAGCTTCTGCTTAGAGAACGGCT 555
Db 491 CTCTCAAGAGGTCTTATTCGTCATCTCAGGAAAGCTTCTGCTTAGAGAACGGCT 550
Qy 556 TTCTGCTGCAATGGACAGAAATCATACAGAGGGCACAGGGCCCTTTCTC 615
Db 551 TTCTGCTGCAATGGACAGAAATCATACAGAGGGCACAGGGCCCTTTCTC 610
Qy 616 ATCGTTTATTCGTCATCTGAGACGCTCTCTGAGGATCTAGTGGCTTTCTCTGGTT 675
Db 611 ATCGTTTATTCGTCATCTGAGACGCTCTCTGAGGATCTAGTGGCTTTCTCTGGTT 670
Qy 676 GGGCATTCTGTCATCTGTCATCTGAGGATCTAGTGGCTTTCTCTGGTTCAAC 735
Db 671 GGGCATTCTGTCATCTGTCATCTGAGGATCTAGTGGCTTTCTCTGGTTCAAC 730
Qy 736 CAGTGGACACAGAGAACCTCACTCTGTAACATGAGGATAGCCGGCCTCTC 795
Db 731 CAGTGGACACAGAGAACCTCACTCTGTAACATGAGGATAGCCGGCCTCTC 790
Qy 796 CAGCACAATCTCTCACTGTTCCACAGCTCTCAGCCACCAAAATAGGCCCTGCTA 855
Db 791 CAGCACAATCTCTCACTGTTCCACAGCTCTCAGCCACCAAAATAGGCCCTGCTA 850

```

ORIGIN

```

RESULT 6
CS02596
LOCUS CS02596
DEFINITION Sequence 2102 from Patent WO2005016962.
ACCESSION CS02596
VERSION GI:60732060
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
1. Abbas, A.; Clark, H.; Ouyang, W.; Williams, M. P.; Wood, W. I. and Wu, T. D.
Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 2005016962-A 2102 24-FEB-2005;
FEATURES Genentech, Inc. (US); Location/Qualifiers 1..1530
Source /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```

ORIGIN

```

Query Match 95.8%; Score 984; DB 6; Length 1530;
Best Local Similarity 98.0%; Pred. No. 4e-242;
Matches 996; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 12 GGGCAAAAATCAAGGTATTGGTCCCGAACAAAGCTATCATACAGATAAACACT 71
Db 515 GGGAAATTATAAGAACCTCTTGGCAGTGACACACTGTGTCAGATAAACACT 574
Qy 72 TGATCGAGATTTCCCAGGCCACTATTTCTCTCATCTGAAACAAAGCT 131
Db 575 TGATCGAGATTTCCCAGGCCACTATTTCTCTCATCTGAAACAAAGCT 634
Qy 132 CCAGAGGCTGGAAACATACCTTGTCTCTTGAGAATTTCCTGATGTATTAGAT 191
Db 635 CCAGAGGCTGGAAACATACCTTGTCTCTTGAGAATTTCCTGATGTATTAGAT 694
Qy 192 ACATGGCAAGAAAGAGAACACAGATCTGGATTCAGGGGAAACCATGAA 251
Db 695 ACATGGCAAGAAAGAGAACACAGATCTGGATTCAGGGGAAACCATGAA 754
Qy 252 GACTAACGACATACATGAAATTAGCTGGTTAACGGTCCAGAAAGTCACTGACAA 311
Db 755 GAATGACGACATACATGAAATTAGCTGGTTAACGGTCCAGAAAGTCACTGACAA 814
Qy 312 AGAACACAGATGATCTGACATGAGAATAAAACGGAGTGTCAAGAATTAT 371
Db 815 AGAACACAGATGATCTGACATGAGAATAAAACGGAGTGTCAAGAATTAT 874
Qy 372 CTTCTCTTAAAGACGAGATGTCATCAATGATCTCCAAAGAACATGTCAGAAGA 431
Db 875 CTTCTCTTAAAGACGAGATGTCATCAATGATCTCCAAAGAACATGTCAGAAGA 934
Qy 432 TGAATGATACACTGTCGCTCAACACCTGCAATTACATGTCATGTCCTCT 491

```

Qy	492	CCTGCTCCCTCAAGAGTGTGCTATTGCCATCATCACCTGTCGCTGCTAGAGAAC	551	Db	TGATGAGATGTTCCCCAACCCACTATTTCTCTGAATAGCTGAACAGCT	634
Qy	995	CCTGCTCCCTCAAGAGTGTGCTATTGCCATCATCACCTGTCGCTGCTAGAGAAC	1054	Db	CGAGAAGCTGCACATACCTGTCCTCTGAGAAATTTCCTCTAGTTAAGAT	191
Qy	552	GCTTCTCTGCAATGGAGAGAACATACACAGGGCAACAGGGCATTCTT	611	Db	ACATGCGAGAAAGAGAGAACAGGATTGGGATCCGGAGGGAACACCTGA	251
Qy	612	CCTCATCGGTATGTCCTAGGAGAACATACACAGGGCAACAGGGCATTCTT	671	Db	ATGGCAAGGAAAGAGAGAACAGGCTTCTGGGATCCGGAGGGAACACCTGA	754
Qy	1115	CCTCATCGGTATGTCCTAGGAGAACATACACAGGGCAACAGGGCATTCTT	1174	Db	GACTAAGACACATACTGAAATTACCTGTTGAGCTTAACGGTCTCTGG	311
Qy	672	GTRGGGCCATTCTAGTTCTATGTTCTACTATTTCTATGTTAAGGTTTC	731	Db	GACTAAGACACATACTGAAATTACCTGTTGAGCTTAACGGTCTCTGG	814
Db	1175	GTTGGGCCATTCTAGTTCTATGTTCTACTATTTCTATGTTAAGGTTTC	1234	Db	AGAACACAGATGTTCTCAGACATGAGAAATTAAACGGGAAACCATGA	371
Qy	732	AAACCACTGGCAACAGAGAACCTACTCTGTTAAACATGAGGAATAGCCACGGGA	791	Db	AGAACACAGATGTTCTCAGACATGAGAAATTAAACGGGAAACCATGA	874
Db	1235	AAACCACTGGCAACAGAGAACCTACTCTGTTAAACATGAGGAATAGCCACGGGA	1294	Db	ATGGCAAGGAAAGAGAGAACAGGCTTCTGGGATCCGGAGGGAACACCTGA	934
Qy	792	TCTCAGGACCAACTCTCTCATGTTTCCACAGCTCTGTTAATGAGGATAGCCACGGGA	851	Qy	TGCAAACTGACACTACTGCTCAGCTCACACACCTCTGATATACATGACCT	491
Db	1295	TCTCAGGACCAACTCTCTCATGTTTCCACAGCTCTGTTAATGAGGATAGCCACGGGA	1354	Db	TGCAAACTGACACTACTGCTCAGCTCACACACCTCTGATATACATGACCT	994
Qy	852	GCTATAGCTAGACATCCCTGGCTCTAGCTTGCCCTCTTAGCTCTTAAATCA	911	Qy	CTCTCCCTCAAATAGGGAGTCACTCACACATGGATCCAAAGACATGTCAAAGA	551
Db	1355	GCTATAGCTAGACATCCCTGGCTCTAGCTCTTAAATCA	1414	Db	CTCTCCCTCAAATAGGGAGTCACTCACACATGGATCCAAAGACATGTCAAAGA	1054
Qy	912	GATAACTGCTGGAGAACCTCTTACACGCCCTGAGAGCAGTCTCTTGCTAGTGA	971	Qy	CTCTCCCTCAAATAGGGAGTCACTCACACATGGATCCAAAGACATGTCAAAGA	1474
Db	1415	GATAACTGCTGGAGAACCTCTTACACGCCCTGAGAGCAGTCTCTTGCTAGTGA	1474	Db	CTCTCCCTCAAATAGGGAGTCACTCACACATGGATCCAAAGACATGTCAAAGA	671
Qy	972	ATATGGTGTGTTTCCGATAATGAAATAATTAAAAAATGAAAGTT	1027	Qy	CTCATCGTTTGTGCTAGGAAATCATACAGGATGTCATCACATGGATCCAAAGACATGTCAAAGA	1174
Db	1475	ATATGGTGTGTTTCCGATAATGAAATAATTAAAAAATGAAAGTT	1530	Db	CTCATCGTTTGTGCTAGGAAATCATACAGGATGTCATCACATGGATCCAAAGACATGTCAAAGA	1234
RESULT 7				Qy	TGATGAGATGTTCCCCAACCCACTATTTCTCTGAATAGCTGAACAGCT	
LOCUS	CS041548	Sequence 2102 from Patent WO200501258.	1530 bp	DEFINITION	DNA	linear
ACCESSION	CS041548			VERSION	PAT 22-MAR-2005	
VERSION	CS041548.1			KEYWORDS		
SOURCE	Homo sapiens (human)			ORGANISM		
REFERENCE	1			REFERENCE		
AUTHORS	Abbas A., Clark H., Ouyang W., Williams P.M., Wood W.I. and Wu T.D.			TITLE		
VERSION				DISABEES		
JOURNAL	Compositions and methods for the treatment of immune related diseases			PATENT		
FEATURES	Patent: WO 200501258-A 2102 03-MAR-2005; Genentech, Inc. (US) Location/Qualifiers			NUMBER		
source	1..-1530			SEQUENCE		
	/organism="Homo Sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
ORIGIN						
Query Match	95.8%	Score 984;	DB 6;	Length 1530;		
Best Local Similarity	98.0%	Pred. No. 4e-242;	Indels 0;	Gaps 0;		
Matches	956;	Conservative	Mismatches 20;			
Db	12	GGCCAAAAATCAGGATTGTCCTGGACAAAGCTTATCATACAGATAAACCT	71	Db	GATAACTGCTGGAGAACCTCTTACACCCCTGAGAGCAGTCTCTTGCTAGTGA	971
Db	515	GGGAAATTATAAGAACCTTTGGAGTGAAACACATGTCAGATAAACCT	574	Db	ATATGGTGTGTTTCCGATAATGAAATAATTAAAAAATGAAAGTT	1027
Qy	72	TGATCAGAGTGTCCCCAACCTATTCTCTCATGTCGAAACAAAGCT	131	Db	ATATGGTGTGTTTCCGATAATGAAATAATTAAAAAATGAAAGTT	1530
RESULT 8				DEFINITION	T-cell receptor gamma chain wjci-cii-ciri region mRNA,	
HOMSTRD				LOCUS	HUMTRGAA	
ACCESSION	M16768			DEFINITION	Human T-cell receptor gamma chain wjci-cii-ciri region mRNA,	
VERSION	M16768.1			complete cds.		
KEYWORDS	T-cell receptor			SOURCE	Homo Sapiens (human)	

		ORGANISM
	Homo sapiens	Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo;
1	(bases 1 to 1530)	Krangel,M.S., Band,H., Rata,S., McLean,J. and Brenner,M.B.
295517	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEIN ENCODED BY DISTINCT C GAMMA GENES	Science 237 (4810), 64-67 (1987)
QY	Original source text:	Human (cell line PBL Cl), cDNA to mRNA, clone PBLCl-15.
PUBMED	Only a few V and J region genes occur within the genome. Diversity in T-cell receptors occur in the V-J recombination events. In some cases, this produces unproductively rearranged reading frames. Also, in some recombination events, some gene regions can be included more than one time creating even more diversity in TCR's.	
COMMENT	Location/Qualifiers	
FEATURES	source	1. . 1530
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/map="7p15-p14"	
gene	1. . 1530	
	/gene="TCRG"	
	<1. . 1530	
	/gene="TCRG"	
	/product="TCR-gamma mRNA"	
CDS	153. . 1085	
	/gene="TCRG"	
	/note="T-cell receptor (V-J-C) precursor"	
	/codon_start=1	
	/protein_id="AA61110_1"	
	/db_xref="GI:339400"	
	/db_xref="GDB:00-120-407"	
	/translation="MISLHAHTLAVIGALCYAGHLQPOISSTKLUKPFLRPLRCV USGMISATSYWRYRGRGIVQPLPSISYDVTRESGIGPKFRUDRPTSTIL TINVEKQDQIATMYCALLEKGKLGTSITLVTKQDADVSPEKTFIPSIATEK LOKAGTCYLICLKEKPFDPVIKHWQEKNTLGSBNTMKNDTYMKPSLUTYPEK YMLYLILKSYFALITCLLRTAFCCNGEKS"	
sig_peptide	153. . 197	
	/gene="TCRG"	
	/note="T-cell receptor signal peptide"	
mat_peptide	198. . 1082	
	/product="TCRG"	
	/gene="TCR-gamma T-cell receptor (V-J-CI-CII-CIII)"	
misc_recomb	517. . 518	
	/gene="TCRG"	
	/organism="Homo sapiens"	
misc_recomb	564. . 565	
	/gene="TCRG"	
	/organism="Homo sapiens"	
misc_recomb	894. . 895	
	/gene="TCRG"	
	/organism="Homo sapiens"	
misc_recomb	942. . 943	
	/gene="TCRG"	
	/organism="Homo sapiens"	
ORIGIN	Chromosome 7p15.	
Query	Match 95.8%; Score 984; DB 8; Length 1530;	
Best Local Similarity 98.0%; Pred. No. 4e-242; Matches 996; Conservative 0; Mismatches 20; Indels 0; Gaps 0;		
Qy	12 GGGCAAAATACTGGATTGCTCCCGAACAAAGCTATCATACAGATAAACACT	71
Db	515 GGGAAATTATAAGAACACTCTTGGCAGTGAACTGTTGCACTAACACT	574
Qy	72 TGTATGAGATGTTCCCCAAGCCCACTTTCTCTCAATGCTGAACAGACT	131
Db	575 TGTATGAGATGTTCCCCAAGCCCACTTTCTCTCAATGCTGAACAGACT	634
RESULT 9		
BC072387	LOCUS	BC072387
	DEFINITION	Homo sapiens T cell receptor gamma variable 9, mRNA (cDNA clone IMAGE:5587705), partial cds.
ACCESSION	VERSION	BC072387.1 GT:47938917
KEYWORDS		
ORGANISM	SOURCE	Homo sapiens (human)
	Homo sapiens	
Rubaryo; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo;		

REFERENCE	
1 ('bases 1 to 1470')	
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B.R., Bustow, K.H., Schaffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H.T., Max, S.I., Wang, J., Heien, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, J., Stapleton, M., Soares, M.B., Boraldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mulley, S.J., Bosak, S.P.H., McEvran, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villanueva, D.K., Muzny, D.M., Sodergreen, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kozlowski, M.I., Skalska, U., Smilus, D.E., Schnarch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REFERENCE	
2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	
TITLE	
JOURNAL	
PUBLISHED	
124(793), 2 (bases 1 to 1470)	
REMARK	
COMMENT	
JOURNAL	
AUTHORS	

RESULT 12

Db 1392 ATGTTTCCACAGCTCCTCAGCCACCAAAATAGCGCTGTATAGTAGACAGCTG 1451
Qy 872 CGGCTTCAGCTTGCTGCCCTCTCTAGTCTTATCATGATACTGCCTGGAGCTT 931
Db 1452 CGCTTCTAGCTCTGCTCCCTCTCTAGTCTTATCATGATACTGCCTGAAGCTT 1511
Qy 932 TCAATTACAGCCCTGAAGCAGCTCTGCTAGTGAATTAGTGGGGTTTCC 991
Db 1512 TCATTTACAGCCCTGAAGCAGCTCTGCTAGTGAATTAGTGGGGTTTCC 1571
Qy 992 GTAAAGCAAAATAATTAAAAAATGAAA 1024
Db 1572 GTAAAGCAAAATAATTAAAAAATGAAA 1604

RESULT 13

Db CQ896252 CQ896252 1421 bp DNA linear PAT 05-NOV-2004
DEFINITION Sequence 76 from Patent WO2004076614.
VERSION CQ896252.1 GI:55468101

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1

AUTHORS Hinzmamn, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Brummendorf, T., Kinnemann, H., Roepcke, S., Hermann, K., Xinzhong, L., Pilarsky, C. and Staub, E.

TITLE Human nucleic acid sequences obtained from prostatic carcinomas
JOURNAL Patent: WO 2004076614-A 76 10-SEP-2004;
Hinzmamn, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE); Specht, Thomas (DE); Schmitt, Armin (DE)

FEATURES source
1. .1421
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 87.8%; Score 902.2; DB 6; Length 1421;
Best Local Similarity 92.8%; Pred. No. 4.5e-221;
Matches 977; Conservative 0; Mismatches 28; Indels 48; Gaps 1;

Db 20 AAATCAGGTTATGGTCCCGGAAACAGCTTATCATTAAGATAAACACTTGATGCA 79
Qy 369 TTAGGAACTCTTGGCAGTGACACCTTGCTGACATGCTGAGTACACTTGAC 428
Db 429 ATGTTTCCCTCAAGCCACTTATTTCCTCATTTCTCATGGAAACAAAGCTCCAGAAG 488
Qy 140 CTGGACATCTCTTGCTTGAGAAATTTCCTGAGTATTAGATACATGCG 199
Db 489 CTGGACATCTCTTGCTTGAGAAATTTCCTGAGTATTAGATACATGCG 548
Qy 200 AGAAAGAAAGACACAGATCTGGATCCAGGAGGGACACCATGAGACTAACG 259
Db 549 AGAAAGAAAGACACAGATCTGGATCCAGGAGGGACACCATGAGACTAACG 608
Qy 260 ACACATACATGAAATTAGCTGGTAACGCTGGCAGAAAGTCATGGACAAAGACAA 319
Db 609 ACACATACATGAAATTAGCTGGTAACGCTGGCAGAAAGTCATGGACAAAGACAA 668
Qy 320 GATGTTGGCAGACTGAGATAAAACGAGTTGATCAAATTCTTCC 379
Db 669 GATGTTGGCAGACTGAGATAAAACGAGTTGATCAAATTCTTCC 728
Qy 380 CAATAAGAC-----GG 391
Db 729 CAATAAGACAGTACACCAGCTGATCCAGACAGTATTCAGAAAGTCGAATG 768

RESULT 13

Db AX32835 AX32835 1421 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3344 from Patent WO0194629.
VERSION AX32835.1 GI:18123469

KEYWORDS

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1

AUTHORS Young, P.E., Augustus, M., Carter, K.C., Einer, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.

TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 3344 13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES source
1. .1421
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 87.8%; Score 902.2; DB 6; Length 1421;

Db 392 ATGTCATCACATGATCCAAAGACAAATGTCAAAGATGCAATGATCAGCTGC 451
Qy 789 ATGTCATCACATGATCCAAAGACAAATGTCAAAGATGCAATGATCAGCTGC 848
Db 452 TCGAGCTACAACACCTCTGCTATTCATGATCAGTACCTGCCTCGCTCAGAGCTGG 511
Qy 849 TCGAGCTACAACACCTCTGCTATTCATGATCAGTACCTGCCTCGCTCAGAGCTGG 908
Db 512 TCATTTGCCATCATGACTGCTGCTGCTGCTGAGAGACGGCTTCCTGCTGAATGGAG 571
Qy 999 TCAATTGCCATCATGCTCTGCTGCTGCTGAGAGACGGCTTCCTGCTGAATGGAG 968

Db 572 AGAAATCAACAGCGGGCAACAGGGCAGCTTTCCTCATCGTTATGTCCT 631
Qy 969 AGAAATCAACAGCGGGCAACAGGGCAGCTTTCCTCATCGTTATGTCCT 1028

Db 632 AGAGGCCTCTGGAGTCTAGTGGCTTTCGGGTTGGSCATTCTGCT 691
Qy 1029 AGAACGCTTCTGGAGGATCTAGTGGCTTTCGGGTTGGCATTCTGCT 1088

Db 692 CATGTGTTACATTCTCATATTGATAACGGTTCAACAGGGCACAGAG 751

Db 1089 CATGTGTTACATTCTCATATTGATAACGGTTCAACAGGGCACAGAG 1148

Db 752 AACCTCACTGTATAACATGAGGATAAGCCACGGGATCTCCAGACAACTCTCC 811
Qy 1149 AACCTCACTGTATAACATGAGGATAAGCCACGGGATCTCCAGACAACTCTCC 1208

Db 812 ATGTTTACAGCTCCCTCAGCAACCCAATAGCGTTCAACAGGGCACAGAG 871
Qy 1209 ATGTTTACAGCTCCCTCAGCAACCCAATAGCGCTGCTGATAGCTGAGCTG 1268

Db 872 CGGTTTACGCTGTGCTCTGTTAGCTCTTAACGATAACTCCTGAGCTT 931

Db 1269 CGGTTCAGCTGTGCTCTGTTAGCTCTTAACGATAACTCCTGAGCTT 1328

Db 932 TCATTTGCCCTGAGCAGCTCTTGTGCTGAGCTT 991

Db 1329 TCATTTACAGCCCTGAGCAGCTCTTGTGCTGAGCTT 1388

Qy 992 GTAAAGCAAAATAATTAAAAAATGAAA 1024

Db 1389 GTAAAGCAAAATAATTAAAAAATGAAA 1421

Best Local Similarity 92.8%; Pred. No. 4_5e-221; Matches 977; Conservative 0; Mismatches 28; Indels 48; Gaps 1;		Db	1389 GTRATAGCCAAATAATTAAAAATGAAA 1421
QY	20 AAATCAAGTTTGGCGCGAACAAAGCTTACATACAGATAAACACTGTATGGAG 79	RESULT 14	RUMTCGXH
Db	369 ATAGAAACTCTTGCGATGAGAACACTTGTGACACTG 428	HUMAN	HUMAN
QY	80 ATGTTTCCCCAACGCCACTATTTCTTCATATGCTAAACAAAGCTTCAAGAGG 139	DEFINITION	Human T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HPB-MLT.
Db	429 ATGTTTCCCCAACGCCACTATTTCTTCATATGCTAAACAAAGCTTCAAGAGG 488	ACCESSION	M13231.1 GI:339168
QY	140 CTGAACTACTCTTGTCTTCTGAGAATTTCCTGATGTTATTAGATACATTGGC 199	VERSION	C-region; J-region; T-cell receptor gamma chain; V-region; antigen receptor; processed gene; pseudogene.
Db	489 CTGGAACTACTCTTGTCTTCTGAGAATTTCCTGATGTTATTAGATACATTGGC 548	SOURCE	Homo sapiens (human)
QY	200 AGAGAAAGAGGACACAGGTTGGATCCAGGGACACCATGAGAACACTAACCG 259	ORGANISM	Homo sapiens
Db	549 AGAAAGAGGACACAGGTTGGATCCAGGGACACCATGAGAACACTAACCG 608	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
QY	260 ACACATACATGAAATTAGCTGTTAACGGTCCAGAAAGTCACTGGACAAAGCA 319	AUTHORS	Dialynas,D.P., Murie,C., Quertermous,T., Boss,J.M., Leiden,J.M., Seidman,J.G. and Strominger,J.L.
Db	609 AACATACATGAAATTAGCTGTTAACGGTCCAGAAAGTCACTGGACAAAGCA 668	TITLE	Cloning and sequence analysis of complementary DNA encoding an aberrantly rearranged human T-cell gamma chain
QY	320 GATGATATCTCAGCATGAGATAAAACGGAGTTGATCAGAAATTACCTTTCCT 379	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 83 (8), 2619-2623 (1986)
Db	669 GATGATATCTCAGCATGAGATAAAACGGAGTTGATCAGAAATTACCTTTCCT 728	COMMENT	Original source text: Human T-cell line HPB-MLT, cDNA to mRNA, clones pR-gamma-[1,2]. Computer-readable sequence of [1] kindly provided by D.P.Dialynas, 31-Oct-1986.
QY	380 CAAATAAGAC-.....GG 391	An aberrant rearrangement at the V-J junction causes a frame shift that leads to peptide termination at the 'aa' codon at positions 370-372.	
Db	729 CAAATAAGACAGATCACCAACAGAATTCAGTAAAG 788	A polyadenylation signal can be found at positions 1400 to 1405.	
QY	392 ATGTCATCACATGATGCCAAAGACAAATGTCAAATGATACACTACTG 451	FEATURES	1. .1421
Db	789 ATGTCATCACATGATGCCAAAGACAAATGTCAAATGATACACTACTG 848	source	/organism="Homo sapiens"
QY	452 TGAAGTCACAACACCTCTGATGAGACAAATGTCAAATGATACACTACTG 511	CDS	/db_xref="Taxon:9608"
Db	849 TGCAGCTCACAAACACCTCTGATGAGACAAATGTCAAATGATACACTACTG 908		4. .979
QY	512 TCTATTTGGCCATCACCTGCTGCTCTAGAGAACGCGTTCTGCTCATGG 571		/note="pseudo" /pseudo
Db	919 TCTATTTGGCCATCACCTGCTGCTCTAGAGAACGCGTTCTGCTCATGG 968		/codon_start=1
QY	572 AGAAATCATCACAGACGGTGGCACAGAGGGCATTTCTCATCGTTATGTCCT 631		4. .63 /note="pseudo-TG signal pept"
Db	969 AGAAATCATCACAGACGGTGGCACAGAGGGCATTTCTCATCGTTATGTCCT 1028		/pseudo /note="pseudo-TG mature pept"
QY	632 AGAGGGCTTCTGAGGTCTGTTGCGCATTTTCAG 691		/pseudo /pseudo
Db	1029 AGAGAGCCTTCTGAGGTCTGTTGCGCATTTTCAG 1088		ORIGIN 16 bp upstream of Apal site; chromosome 7.
QY	692 CATGTGTGACTATCTCATATTGATAACGGTTCAAAACAGTGGACACAG 751		Query Match 87.8%; Score 902.2; DB 8; Length 1421; Best local Similarity 92.8%; Pred. No. 4_5e-221; Matches 977; Conservative 0; Mismatches 28; Indels 48; Gaps 1;
Db	1029 CATGTGTGACTATCTCATATTGATAACGGTTCAAAACAGTGGACACAG 1148		Matches 977; Conservative 0; Mismatches 28; Indels 48; Gaps 1;
QY	752 AACCTCAGCTCTGTTAACTAACATGAGAATTAGCCAGGGCATTCAGCAACCAACTCTCTC 811		QY 20 AAATCAAGGTTGTCGGCGAACAAAGCTTACATCATACAGATAAACACTGTGAG 79
Db	1149 AACCTCAGCTGTTAACTAACATGAGAATTAGCCAGGGCATTCAGCAACCAACTCTC 1208		Db 369 ATAGAAACTCTTGCGGTGGACAAACACTGTGTCACAGATAAACACTGTGAG 428
QY	812 ATGTTTCCACAGCTTCCAGAACCAAATAGCGCTGTTACAGATAACTGCTGAGCT 871		QY 80 ATGTTTCCCCAACGCCACTATTTCTCTCTCAATGCTGAGAACAGCTCAGAGG 139
Db	1209 ATGTTTCCACAGCTTCCAGAACCAAATAGCGCTGTTACAGATAACTGCTGAGCT 1268		Db 429 ATGTTTCCCCAACGCCACTATTTCTCTCTCAATGCTGAGAACAGCTCAGAGG 488
QY	872 CGGTCTCAGCTGTTCCCTCTCTAGTTCTTAACTAGATAACTGCTGAGCT 931		QY 140 CTGGAACTACTCTTGTCTTCTGAGAATTTCCTGATGTTATTAGATACATTGGC 199
Db	1269 CGACTCTCTGCTGCTCTCTAGTTCTTAACTAGATAACTGCTGAGCT 11328		Db 489 CTGGAACTACTCTTGTCTTCTGAGAATTTCCTGATGTTATTAGATACATTGGC 548
QY	932 TCAATTACAGGCCCTGAAAGAGCTCTTGTCTGAGAATTTCCTGATGTTATTAGATACATTGGC 991		QY 200 AACGAAAGAGGACACCGATTCGGATCCAGGGAGAACCTGAGACTACAG 259
Db	1329 TCATTACAGGCCCTGAAAGAGCTCTTGTCTGAGAATTTCCTGATGTTATTAGATACATTGGC 1388		Db 549 AACGAAAGAGGACACCGATTCGGATCCAGGGAGAACCTGAGACTACAG 608
QY	992 GTAAATGAAATAATTAAAAATGAAA 1024		QY 250 AACATACATGAAATTGCTGCTGCTGCTGAGAGGACTGAGACTGAGACACA 319
			Db 649 AACATACATGAAATTGCTGCTGCTGAGAGGACTGAGACTGAGACACA 668

	COMMENT	On Sep 21, 1994 this sequence version replaced gi_34169. Original Source text: Homo sapiens PHA-stimulated peripheral T cell cDNA to mRNA.
	FEATURES	source
QY		1..1013
Db		/organism="Homo sapiens"
QY		/mol_type="mRNA"
Db		/db_xref="Taxon: 9606"
QY		/map="P15_P14"
Db		/clone="HG08"
QY		/tissue_type="PHA-stimulated peripheral T cell"
Db		1..1013
QY		/gene="TCRG2"
Db		<1..570
QY		/note="This CDS feature is included to show the translation of the corresponding C_region features are illegal."
Db		/protein_id="AA6112.1"
QY		/product="T cell receptor gamma chain"
Db		/translation="DKOLDAWSPKPFLPSIAETKQAGTYLCLKEKPPDIIKHNOKSNTLGSQEGNTYKFSWLTYPESLDKSHRCVHRNNKGIDIELIFFPIKUDTTVDPKNYSKDANDVTDMDPKUNWSKDNNTLQLINTTAYMILLIJKSVVYFAIITCCILGRTAFCNCBKS"
QY		<1..570
Db		/gene="TCRG2"
QY		/note="G00-120-409"
Db		1013
QY		/note="G00-120-409"
Db		969..994
QY		/note="G00-120-409"
Db		1208
QY		ORIGIN
Db		Query Match 85.4%; Score 877.4; DB 8; Length 1013;
QY		Best Local Similarity 94.0%; Pred. No. 1..e-214; Matches 954; Conservative 0; Mismatches 11; Indels 50; Gaps 2;
Db		931
QY		931
Db		1228
QY		932
Db		1329
QY		932
Db		1308
QY		992
Db		1389
QY		992
Db		1421
RESULT 15		
HUMTCRGAA		
DEFINITION		1013 bp mRNA linear PRI 14-JAN-1995
Homo sapiens (clone HGP08) T cell receptor gamma-chain mRNA, C2 region.		
ACCESSION		M27331
VERSION		M27331.1 GI:540458
KEYWORDS		T cell receptor gamma-chain; constant region.
SOURCE		(bases 1 to 1013)
ORGANISM		Homo sapiens
REFERENCE		Yoshikai, Y., Toyonaga, B., Koga, Y., Kimura, N., Griesser, H. and Mak, T.W.
AUTHORS		Bukaroyta, Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchoptoglires; Primates; Catarrhini; Hominoidea; Homo.
TITLE		Repertoire of the human T cell gamma genes: high frequency of nonfunctional transcripts in thymus and mature T cells
JOURNAL		Eur. J. Immunol. 17 (1), 119-126 (1987)
PUBLMED		2949984

QY	493	CTGCCTCCAAAGAGTGTGCTTATTTGCCATCATCACCTGTCGTCCTGAGAACG	5 552
Db	481	CTGCCTCCAAAGAGTGTGCTTATTTGCCATCATCACCTGTCGTCCTGAGAACG	5 540
QY	553	GCTTCCTGCTGCAATGGAGAGAAATCATACAGACGGGGCAAGAGGGCCTCTTC	6 612
Db	541	GCTTCCTGCTGCAATGGAGAGAAATCATACAGACGGGGCAAGAGGGCCTCTTC	6 600
QY	613	CTCATCGGTTATTCCTCTAGAAGCGTCCTCGAGGACTAATGGGCTTCCTTCGG	6 672
Db	601	CTCATCGGTTATTCCTCTAGAAGCGTCCTCGAGGACTAATGGGCTTCCTTCGG	6 660
QY	673	TTGGGCCATTCTGTTCTGTTGACTCTCTATCATATATGATAACGGTTCA	7 732
Db	661	TTGGCCATTCTGTTCTGTTGACTCTCTATCATATATGATAACGGTTCA	7 718
QY	733	AACCAAGTGGCACACAGAGAACCTACTCTGTAATACATGAGGAATAGCAGGGCAT	7 792
Db	719	AACCAAGTGGCACACAGAGAACCTACTCTGTAATACATGAGGAATAGCAGGGCAT	7 778
QY	793	CTCCAGCACAATCTCCATGTTTCCACAGGCTCCAGGACCCAAATAGGGCTG	8 852
Db	779	CTCCAGCACAATCTCCATGTTTCCACAGGCTCCAGGACCCAAATAGGGCTG	8 838
QY	853	CTATAGTGTAGCATCTCGCGCTCTAGCCCTGCCCCTCTAGTGTCTTATCAG	9 912
Db	839	CTATAGTGTAGCAGCCCTCGCTGCTGCTTCTCTAGTGTCTTATCAG	9 898
QY	913	ATTAAGTGCCTGGAAGCCTTCAATTACAGCCCTGAAAGCAGCTCTCTGTGTTCAA	9 972
Db	899	ATTAAGTGCCTGGAAGCCTTCAATTACAGCCCTGAAAGCAGCTCTCTGTGTTCAA	9 958
QY	973	TATGTGGTGTGTTCTGTTAGCAATAATTAAAGATGAAAGTT	10 1027
Db	959	TATGTGGTGTGTTCTGTTAGCAATAATTAAAGATGAAAGTT	10 1013

Search completed: December 10, 2005, 22:14:55
 Job time : 5319 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 8, 2004, 06:11:46 ; Search time 1877 Seconds
(without alignments)
1461.269 Million cell updates/sec

Title: US-10-031-158-14

Perfect score: 307

Sequence: 1 MQMFPSSPLFFPLQLLKKQSS.....RYIGKRRATRFWDPRRGTP 58

Scoring table:

BLOSUM62 Xgapext 0.0 , Ygapext 0.5
Ygapop 1.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2n.model -DEV=xlh
-MODELF=frame+P2n.model -DEV=xlh/runat_06122004_08265919887/app/query.fasta_1.199
-Q=/cgn2.1/USPPro/spool/US10031158/runat_06122004_08265919887/app/query.fasta_1.199
-DB=GenEmbl -ORFM=-fastap -SUFFIX=seq -MINMATCH=0.1 -LOCOPCT=0 -LOCOPCTN=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=80 -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTPFT=txt -NORM=ext -HBBPSIZE=50 -MINLEN=2000000000 -MAXLEN=2000000000
-USER=US10031158@cgn1.1-2527@runat_06122004_082659_15887 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NNG SCORES=0 -WAIT -DBPBLOCK=100 -LONGLOG
-DEV TIMEOUT=20 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOPT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl,*
1: gb_baa:*

2: gb_htg:*

3: gb_mim:*

4: gb_om:*

5: gb_ovr:*

6: gb_pat:*

7: gb_ph:*

8: gb_p1:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
HUMTCGCD1 HUMTCGCD1
LOCUS HUMTCGCD1
DEFINITION Human T-cell receptor germline gamma-chain (TCRGCl) gene,
CL-region, exon 1.
ACCESSION M14996
VERSION M14996.1
KEYWORDS C-region; T cell receptor gamma-chain; T-cell receptor; germline.
SEGMENT 1 of 3
SOURCE Homo Sapiens (human)
ORGANISM Homo Sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.
1 (bases 1 to 410)
REFRANC, M.P., FORSTER, A. and RABBITS, T.H.
Genetic polymorphism and exon changes of the constant regions of the human T-cell rearranging gene gamma
Proc. Natl. Acad. Sci. U.S.A. 83 (24), 9596-9600 (1986)

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	307	100.0	410	HUMTCGCD1
2	307	100.0	426	AX884816 Sequence
3	307	100.0	426	BD02426 Sequence
4	307	100.0	470	CQ131517 Sequence

FEATURES source
1..410
/organism="Homo Sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

COMMENT
Original source text: Homo sapiens (clone: lambda-D19) DNA.
Entry revisions for [1] kindly provided by M.-P. Lefranc,
22-JUN-1988.
Location/Qualifiers

ACCESSION CQ131517
VERSION CQ131517.1 GI:41088873
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Cattarrhini; Hominidae; Homo.
REFERENCE 1 Penn, S. G., Hanzel, D. K., Chen, W. and Rank, D. R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human bone marrow
JOURNAL Patent: WO 015276-A 1539 09-AUG-2001;
Acomica, Inc. (US)
FEATURES source
1. -470 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AF159056.1-EXPRESSED IN BONE MARROW, SIGNAL
= 2.2"
ORIGIN
Alignment Scores:
Pred. No.: 4.16e-30 Length: 470
Score: 3.07.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-031-158-14 (1-58) x CQ131517 (1-470)
QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGinSer 20
Db 203 ATGCAGATGTTCGCCAGCCACTATTTCTTCTCAATTGCTAACAAAGCTCC 262
QY 21 ArgArgLeuGluLisThrPheValPheLeuAqAsnPieSerIeuMetLeuLeuArgTyr 40
Db 263 AGGGCTGGACATACCTTGCTCTCTGAGAAATTTCCTGATGTTATAGATC 322
QY 41 IleGlyLysSarGalaThrArgPheTrpAspProArgArgGlyThrPro 58
Db 323 ATTGGCAAGAAGAAGAGACAGCACAGGATCTGGATCCAGGGAGACACCA 376
RESULT 6
CQ132293
LOCUS CQ132293 Sequence 2315 from Patent WO015276. 477 bp DNA linear PAT 21-JAN-2004
DEFINITION
ACCESSION CQ132293
VERSION CQ132293.1 GI:41088649
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cattarrhini; Hominidae; Homo.
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human bone marrow
JOURNAL Patent: WO 015276-A 2315 09 AUG-2001;
Acomica, Inc. (US)
FEATURES source
1. -477 /organism="Homo sapienB"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AF159056.1-EXPRESSED IN BONE MARROW, SIGNAL
= 1.4"
ORIGIN
Alignment Scores:
Pred. No.: 4.23e-30 Length: 477
Score: 3.07.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-031-158-14 (1-58) x CQ132293 (1-477)
QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGinSer 20
Db 212 ATGCAGATGTTCGCCAGCCACTATTTCTTCTCAATTGCTAACAAAGCTCC 271
QY 21 ArgArgLeuGluLisThrPheValPheLeuAqAsnPieSerIeuMetLeuLeuArgTyr 40
Db 272 AGGGCTGGACATACCTTGCTCTCTGAGAAATTTCCTGATGTTATAGATC 331
QY 41 IleGlyLysSarGalaThrArgPheTrpAspProArgArgGlyThrPro 58
Db 332 ATTGGCAAGAAGAAGAGACAGCACAGGATCTGGATCCAGGGAGACACCA 385
RESULT 7
CQ200006
LOCUS CQ200006 Sequence 2283 from Patent WO15271. 477 bp DNA linear PAT 21-JAN-2004
DEFINITION
ACCESSION CQ200006
VERSION CQ200006.1 GI:41185670
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cattarrini; Hominidae; Homo.

REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human breast and bt 474 cells
PATENT: WO 0157271-A 2283 09-AUG-2001;
JOURNAL Aeonica, Inc. (US)

FEATURES Location/Qualifiers

1. 477 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AF159056.1~EXPRESSED IN BT474, SIGNAL = 1.1"

ORIGIN

Alignment Scores:
Pred. No.: 4.23e-30
Score: 307.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6 Gaps:

Length: 477
Matches: 58
Conservative: 0
Mismatches: 0
Indels: 0

us-10-031-158-14 (1-58) x CQ291096 (1-477)

Qy 1 MetGlmMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuGlnSerSer 20
Db 212 ATGAGATGTTCCCCAACGCCACTATTTCCTCATGGTCAATGCTGAAACAGCTCC 271

Qy 21 ArgArgLeuGluHiThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
Db 272 AGAGGCTGGACATACCTTGCTCTTGAGAAATTTCCTGTGATGTTATTAGATAC 331

Qy 41 IleGlyLysIysAArgGalaIleArgPheTrpAspProArgArgGlyThrPro 58
Db 332 ATTGGCAAGAAAGAGCACACGGATTCCAGAGGGACACCA 385

RESULT 9
CQ490917/c
LOCUS CQ490917
DEFINITION Sequence 539 bp DNA linear PAT 30-JAN-2004
VERSION CQ490917
ACCESION CQ490917
VERSION CQ490917.1 GI:41456536

REFERENCE Schlegel, R., Endege, W.O. and Monahan, J.B.
AUTHORS TITLE Genes differentially expressed in human prostate cancer and their
KEYWORDS SOURCE use
JOURNAL Millennium Predictive Medicine, Inc. (US)
PATENT: WO 0160860-A 22784 23-AUG-2001;

FEATURES /organism="Homo sapiens"
SOURCE /mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 4.84e-30
Score: 307.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6 Gaps:

Length: 539
Matches: 58
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

us-10-031-158-14 (1-58) x CQ490917 (1-539)

Qy 1 MetGlmMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuGlnSerSer 20
Db 410 ATGCAGATGTTCCCCAACGCCACTATTTCCTCATGGTCAATGCTGAAACAGCTCC 351

Qy 21 ArgArgLeuGluHiThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
Db 350 AGAGGCTGGACATACCTTGCTCTTGAGAAATTTCCTGTGATGTTATTAGATAC 291

Qy 41 IleGlyLysIysAArgGalaIleArgPheTrpAspProArgArgGlyThrPro 58
Db 290 ATTGGCAAGAAAGAGCACACGGATTCCAGAGGGACACCA 237

RESULT 10
CQ496769/c
LOCUS CQ496769
DEFINITION Sequence 539 bp DNA linear PAT 30-JAN-2004
VERSION CQ496769
ACCESION CQ496769
VERSION CQ496769.1 GI:41462398

REFERENCE Schlegel, R., Endege, W.O. and Monahan, J.B.
AUTHORS

Alignment Scores:
Pred. No.: 4.223e-30
Score: 307.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6 Gaps:

Length: 477
Matches: 58
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

ORIGIN
/note="MAP TO AF159056.1~EXPRESSED IN LUNG, SIGNAL = 5.3"

Alignment Scores:
Pred. No.: 4.223e-30
Score: 307.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6 Gaps:

Length: 477
Matches: 58
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0103060-A 28635 23-AUG-2001;
FEATURES SOURCE Millennium Predictive Medicine, Inc. (US)
LOCATION/Qualifiers location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.:	4.84e-30	Length:	539
Score:	307.00	Matches:	58
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-031-158-14 (1-58) x CQ496769 (1-539)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnIleLeuLeuLysGlnSerSer 20
Db 410 ATGCAGATGTTTCCCGAACGCCACTATTTCCTCTCAATGCTGAAACAGCTC 351

QY 21 ArgArgLeuLysIthrPheValPheLeuArgSerLeuMetLeuLeuArgTyr 40
Db 350 AGAAAGCTGGACACATACCTTGTCTCTGAGAATTTCCTCTGATGTATAGATAC 291

QY 41 IleGlyLysArgArgAlaThrArgProTrpAspProArgArgGlyLysThrPro 58
Db 290 ATTGGCAAGAAAGAGAGCACACGATCTGGATCCCGAGGGAACACCA 237

RESULT 11

AJ583012

LOCUS AJ583012

DEFINITION Homo sapiens partial mRNA for T-cell receptor gamma chain (TCRG gene), clone 15.1.21.Bob.

ACCESSION AJ583012

VERSION AJ583012.1

KEYWORDS T-cell receptor gamma chain; TCRG gene.

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Green,A.E., Lissina,A., Hutchinson,S.L., Temple,B., Boulter,J.M., Price,D.A. and Sewell,A.K.

AUTHORS Price,D.A. and Sewell,A.K.

TITLE Recognition of non-peptide antigens by human Vgamma9 Vdelta2 TCRs requires contact with a cell of human origin

REFERENCE 2 (bases 1 to 723)

AUTHORS Green,A.E.

TITLE Direct Submission

JOURNAL Submitted (16-SEP-2003) Green,A.E., Nuffield Department of Medicine, University of Oxford, Peter Medawar Building, South Parks Rd, Oxford, OX1 3SY, UNITED KINGDOM

FEATURES SOURCE

1. .723	/organism="Homo sapiens"
/mol_type="mRNA"	/db_xref="taxon:9606"
/clone="15.1.21.Bob"	/cell_type="gamma/delta T cell"
/rearranged	

gene

1. .723

/gene="TCRG"

1. .723

/gene="TCRG"

/codon_start=1

/evidence=experimental

/product="T-cell receptor gamma chain"

/protein_id="C4E47524.1"

/protein_id="C4E47524.1"

ORIGIN

V_region

J_segment

C_region

ORIGIN

Alignment Scores:

Pred. No.:	6.72e-30	Length:	723
Score:	307.00	Matches:	58
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-031-158-14 (1-58) x AJ583012 (1-723)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnIleLeuLeuLysGlnSerSer 20
Db 377 ATGCAGATGTTTCCCGAACGCCACTATTTCCTCTGATGTATAGATAC 436

QY 21 ArgArgLeuLysIthrPheValPheLeuArgSerLeuMetLeuLeuArgTyr 40
Db 437 AGAAGCTGGACACATACCTTGTCTCTGAGAATTTCCTCTGATGTATAGATAC 496

QY 41 IleGlyLysArgArgAlaThrArgProTrpAspProArgArgGlyLysThrPro 58
Db 497 ATTGGCAAGAAAGAGAGCACACGATCTGGAGATCCCGAGGGAACACCA 550

RESULT 12

AJ583014

LOCUS AJ583014

DEFINITION Homo sapiens partial mRNA for T-cell receptor gamma chain (TCRG gene), clone 16.1.2.Wendy.

ACCESSION AJ583014

VERSION AJ583014.1

KEYWORDS T-cell receptor gamma chain; TCRG gene.

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Green,A.E., Lissina,A., Hutchinson,S.L., Temple,B., Boulter,J.M., Price,D.A. and Sewell,A.K.

AUTHORS Price,D.A. and Sewell,A.K.

TITLE Recognition of non-peptide antigens by human Vgamma9 Vdelta2 TCRs requires contact with a cell of human origin

REFERENCE 2 (bases 1 to 726)

AUTHORS Green,A.E.

TITLE Direct Submission

JOURNAL Submitted (16-SEP-2003) Green,A.E., Nuffield Department of Medicine, University of Oxford, Peter Medawar Building, South Parks Rd, Oxford, OX1 3SY, UNITED KINGDOM

FEATURES SOURCE

1. .726	/organism="Homo sapiens"
/mol_type="mRNA"	/db_xref="taxon:9606"
/clone="16.1.2.Wendy"	/cell_type="gamma/delta T cell"
/rearranged	

gene

1. .726

/gene="TCRG"

CDS

- >726
/gene="TCRG"
/codon_start=1
/product="T-cell receptor gamma chain"
/protein_id="CAB47526.1"
/db_xref="GI:31749411"
/translation="MAGHLRPOISSTKLSKARLECWVGSGITATSVWYRERPG
EVIQFLVSIYDGTVRKSGIPSKFEDRIPSTSTLTHNEVKODIATYCALME
VTEGKKTRVFGTKLIDQPKDADYSKPPTFLPPIAETKLQKAGTYCILKEFP
PDVKTHMOKKSNTLGSORGNTNDYTMKRSWLTVPEBSDLKHEHRCIVRNENK
NGVDQEIIFFPIKDVITMDPKDN"

V_region

- . .39
/gene="TCRG"
/note="TRGV9"
/note="TCRG"
/note="TRGJP"
/note="TRGJ"
/note="TRGCL"

ORIGIN

Alignment Scores:
Pred. No.: 6.76e-30 Length: 726
Score: 307.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9 Indels: 0
DB: Gaps: 0

RESULT 13

US-10-031-158-14 (1-58) x 189883 (1-825)

QY 1 MetGlnMetPheProProSerProleuPhePhePhePheAlaGlnLeuLeuIgYglnSerSer 20
Db 380 ATGCAGATGTTCCCCAACGCCACTATTCTCTCATGGAAACAAAGCTC 439

QY 21 ArgArgLeuGluIleThrLeuValPheLeuArgAsnPheSerIleLeuArgTyr 40
Db 440 AGAGGCTGGACATCCCTTGCTCTTGAGAAATTTCCTGTGATGTTAAGATAC 499

QY 41 IleGlyLysIleSargArgAlaThrArgPheTrpAspProArgArgLysPro 58
Db 500 ATTGGCAGAAAAGAGCACACCGATCTGGATCCACAGAGGGACACCA 553

RESULT 14

HSTRGSA HSTRGSA mRNA for soluble gamma TCR. linear PRI 09-SEP-1993

LOCUS H_sapiens mRNA for soluble gamma TCR.
DEFINITION H_sapiens mRNA for soluble gamma TCR.
ACCESSION X72500
VERSION X72500.1 GI:299106
KEYWORDS soluble receptor; T cell receptor gamma chain.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

JOURNAL J. Biol. Chem. 268 (21), 15455-15460 (1993)

REFERENCE 9334040
AUTHORS 8340374
PUBMED 2 (bases 1 to 825)

REFERENCE Davodeau, F.
AUTHORS Davodeau, F., Boulot, G., Romagne, F., Necker, A., Canavo, N., Peyrat, M.A., Hallet, M.M., Vie, H., Jacques, Y., Mariuzza, R. and Bonneville, M.

FEATURES secretion of disulfide-linked human T-cell receptor gamma delta heterodimers

JOURNAL Direct Submission
SUBMITTED (28-APR-1993) F. Davodeau, INSERM U211, Institut de Biologie, 9 Quai Moncousu, 44035 Nantes Cedex 01, FRANCE

JOURNAL Location/Qualifiers 1. .825

source /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="7"
/map="q15"
/tissue_type="blood"
/cell_type="T lymphocyte"
/codon_start=1
/product="gamma-delta T-cell receptor"
/protein_id="CAAS1165.1"
/db_xref="GI:298107"
/translation="MSLILHASTLAVLGALCVGAGHLEQPOISSTKLSKARLECYVSGITISVYWRERPGEVQLVSIYDGTVRKSGIPSKFEDRIPSTSTLTHNEVKODIATYCALMEVTEGKKTRVFGTKLIDQPKDADYSKPPTFLPPIAETKLQKAGTYCILKEFPDVKTHMOKKSNTLGSORGNTNDYTMKRSWLTVPEBSDLKHEHRCIVRNENKNGVDQEIIFFPIKDVITMDPKDN"

V_segment

- . .364
N_region
J_segment
C_region
/product="V-gamma-9"
/product="V-gamma-9"
/product="J-gamma-P"
/product="C-gamma"

ORIGIN

Alignment Scores:
Pred. No.: 7.79e-30 Length: 825
Score: 307.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6 Indels: 0
DB: Gaps: 0

RESULT 15

US-10-031-158-14 (1-58) x 189883 (1-825)

QY 1 MetGlnMetPheProProSerProleuPhePhePheAlaGlnLeuLeuIgYglnSerSer 20
Db 440 ATGCAGATGTTCCCCAACGCCACTATTCTCTCATGGAAACAAAGCTC 499

QY 21 ArgArgLeuGluIleThrLeuValPheLeuArgAsnPheSerIleLeuArgTyr 40
Db 500 AGAGGCTGGACATACCTTGCTCTTGAGAAATTTCCTGTGATGTTAAGATAC 559

QY 41 IleGlyLysIleSargArgAlaThrArgPheTrpAspProArgArgLysPro 58
Db 560 ATTGGCAGAAAAGAGCACACCGATCTGGATCCACAGAGGGACACCA 613

info@cgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fiell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Krzywinski, Reta Kutschke, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Jiisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smilus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Nataesja van den Bosch, Jill Vardy,
 George Yang, Scott Zyderdlyn, Marco Marra.

Clone distribution: MGCC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAL Plate: 51 Row: e Column: 16
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

FEATURES SOURCE

Location/Qualifiers
 1..1054

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:424893"

/tissue_type="prostate"

/clone_Tib="NIR MCG_83"

/lab_host="DHU0B"

/note="vector: pDNR-LIB"

<1..1054

/gene="TRGV9"

/note="synonyms: TCGRV9, V2"

/db_xref="IMGT/LIGM:TRGV9"

/db_xref="LocusID:6983"

1..577

/gene="TRGV9"

/codon_start=2

/product="TRGV9 protein"

/protein_id="AAH62761_1"

/db_xref="IMGT/LIGM:TRGV9"

/db_xref="LocusID:6983"

/translation="GGQRKIKVFGPGPKLILTDQQLDAVDSPKPTIFLPSTAETKLK

AGTYCLLKEPFDFDVKIKHWEQKSNTLGSORGNTMTNDTMMKFSLNTVEKSLDK

ERCTVRENKNGYDTEPPTIVDTWPKDNESKDANDTLLQLWTNSAAYMK

LULILKSVTFALTICLRLRRAFCNGEKS"

74..364

/gene="TRGV9"

/note="TRGV9"

/subfamily="

/db_xref="CDD:cd00098"

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-29

Length: 1054

Matches: 58

Conservative: 0

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 6

Gaps: 0

US-10-031-158-14 (1-58) x CQ493215 (1-1316)

QY 1 MetGlnMetPheProProSerProLeuPhePhePhePhePhePheLeuGlnLeuLeuLeuGlyGlnSerSer 20

Db 562 ATGAGAGATTCCCGAACGCCACTATTTCTCTCAATTGCTTCAGTAACTGCTTACAAAGCTCC 503

QY 21 ArgArgLeuGluIleThrPheValPheLeuArgSerLeuMetLeuLeuArgTrp 40

Db 502 AGAGGGCTGAGACTACCTCTGCTCTGAGAAATTCTCCGATGATGATAGATAC 443

QY 41 IleGlyLeuValBargArgAlaIleArgPheTrpAspProArgArgGlyThrPro 58

Db 442 ATTGGCAAGAAAGAGAGCAACAGATCTGGGATCCCCAGGGAGGACACCA 389

RESULT 20

CQ94607/c

LOCUS CQ94607

DEFINITION Sequence 26474 from Patent WO160860.

ACCESSION CQ94607

VERSION CQ94607.1 GI:41460226

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Schlegel,R., Endge,W.O. and Monahan,J.B.

AUTHORS Genes differentially expressed in human prostate cancer and their

use

JOURNAL Patent: WO 0160860-A 26474 23-AUG-2001;

FEATURES Millennium Predictive Medicine, Inc. (US)

ORIGIN

Alignment Scores:

Pred. No.: 1.31e-29

Length: 1316

Matches: 58

Conservative: 0

Percent Similarity: 100.00%

Score: 1.31e-29

Source: /organism="Homo sapiens"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 307.00

Length: 1316

Matches: 58

Conservative: 0

Percent Similarity: 100.00%

Score: 307.00

Source: /organism="Homo sapiens"

/db_xref="taxon:9606"

RESULT 19

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-031-158-14 (1-58) x CQ494607 (1-1316)			
QY	1 MetGlnMetPheProProSerProleuPhePhePheLeuGlnLeuLeuIysGlnSerSer	20	Dietrich, N.L., Granite, S., Guan, X., Gupta, J.J., Haghghi, P., Hansen, N., Ho, S.-L., Karlin, E., Kong, P., Leric, P., Logaspi, R., Maduro, O.L., Maniello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantic-Pop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.J., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.
Db	562 ATGCAGATGTTTCCCCAACGCCACTATTTCCTCTCAATTCTGAAACAAAGCTCC	450	
QY	21 ArgArgLeuGluHiThrPheValPheLeuArgAsnPheserLeuMetLeuLeuArgTYR	40	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
Db	502 AGAAGGCTGAAACATACCTTGCTCTGAGAAATTTCCTCGATGTATTAGATAC	443	Series: IRAX Plate: 174 Row: a Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
QY	41 IleGlyIysLysSargArgAlaThrArgPhePheLeuArgAsnPheserLeuMetLeuLeuArgTYR	58	Location/Qualifiers
Db	442 ATGGCAAGAAGAAGAGAGAGCAGATCTGGATCCAGGGAGACCA	389	1. .1470
RESULT 21			/organism="Homo sapiens"
BC072387	BC072387	1470 bp mRNA linear	/mol_type="mRNA"
LOCUS	Homo sapiens T cell receptor gamma variable 9, mRNA (cdna clone IMAGE:5587705), partial cds.	PRI 30-JUN-2004	/db_xref="IMGT/LIGM:TRGV9"
DEFINITION			/note="Vector: pCMV-SPORT6"
IMAGE:5587705			/note="clone ID=NIH MGC_25"
ACCESSION	BC072387		/note="Lab host=DH10B"
VERSION	BC072387.1	GI:47938917	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Bukarvata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
REFERENCE			
AUTHORS	1. (bases 1 to 1470)		
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemesh, C.M., Schuler, G.D., Altenschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stippleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheckter, T.E., Brownstein, M.J., Usdin, Y., Toshiyuki, S., Caminchi, P., Prange, C.E., Rana, S.S., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Boak, S.A., McEwan, P.J., Mertzman, K.J., Malek, J.A., Gunnarne, P.H., Richards, S., Wolley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fabley, J., Heitton, E., Ketteman, M., Maden, A., Rodrigues, S., Sanchez, A., Whiting, M., Maden, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smialius, D.E., Scheinrich, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
REFERENCE	1247932		
AUTHORS	2. (bases 1 to 1470)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission		
COMMENT	Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncbi.nih.gov		
REMARK	Contact: MGC help desk		
REMARK	Email: cgabps-r@mail.nih.gov		
REMARK	Tissue Procurement: Invitrogen		
REMARK	cDNA Library Preparation: Life Technologies, Inc.		
REMARK	cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LILN)		
REMARK	DNA Sequencing By: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;		
REMARK	Web site: http://www.nisc.nih.gov/		
REMARK	Contact: nisc_mgc@hgmr.nih.gov		
REMARK	Aktier, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,		
RESULT 22			
HUMTCRGA	391 ATGCAGATGTTCCCCAACGCCACTATTTCCTCTCAATTCTGAAACAAAGCTCC	450	
LOCUS			
DEFINITION	Human T-cell receptor gamma chain VU-CII-CII region mRNA, complete cds.		
ACCESSION	M16768		
VERSION	M16768.1	GI:339399	

Clone distribution: MCC clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: TRAK Plate: 174 Row: c Column: 15
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES Location/Qualifiers
 SOURCE

1. . 1825
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:90486 IMAGE:575352"
 /tissue="Blood, adult leukocytes"
 /clone_id="NIH_MGC_118"
 /lab_host="DIII0B"
 /note="vector: pCMV-SPORT6"
 1. . 1825
 /gene="TRGV9"
 /note="SYNonyms: TRGV9, V2"
 /db_xref="GI:47939859"
 /db_xref="LocusID:6983"
 376..1325
 /gene="TRGV9"
 /codon_start=1
 /product="TRGV9 protein"
 /protein_id="AAH73396.1"
 /db_xref="IMGT/LIGM:TRGV9"
 /db_xref="LocusID:6983"
 /translators="MSI.UHTSTIAVGLCAGAGHUBOPOLSKTLSPARLBCV
 VSGTISATSYWVYRPECVTIVLVSIGRPSKKEVDRIPENSTSL
 TIRNEVKODIATTCALMEVFGSEIGKCKKUFGEGKLUITDQEGMTKNDTYMKFSWL
 IAEFKLQKAGTYLQLKEPKDVKIHBEKKNTLGSOEGRNTKNDTYMKFSWL
 VPESLSDKHEHRCTYRNKGKQDELEPPKTDMDPKONCSKDADTLLQLT
 NTSAVITYTYLILNGSVVFAITCCLRRTAFCGNGERS"

ORIGIN

Alignment Scores:
 Pred. No.: 1.89e-29 Length: 1825
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9 Indels: 0
 DB: Gaps: 0

US-10-031-158-14 (1-58) x BC072396 (1-1825)

CDS

TITLE

JOURNAL

COMMENT

AII repeats were identified using RepeatMasker:
<http://www-genome.wi.mit.edu/RM/RepeatMasker.html>

----- Project Information

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Direct Submission

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:
<http://www-genome.wi.mit.edu/RM/RepeatMasker.html>

----- Project Information

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Direct Submission

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:
<http://www-genome.wi.mit.edu/RM/RepeatMasker.html>

----- Project Information

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Direct Submission

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:
<http://www-genome.wi.mit.edu/RM/RepeatMasker.html>

----- Project Information

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

* NOTE: This record contains 80 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

* 1. 735: contig of 735 bp in length
 * 736: gap of 100 bp
 * 835: contig of 737 bp in length
 * 1573: gap of 100 bp
 * 1672: gap of 100 bp
 * 2399: contig of 727 bp in length
 * 2400: gap of 100 bp
 * 2500: contig of 721 bp in length
 * 3220: gap of 100 bp
 * 3321: contig of 717 bp in length
 * 4038: gap of 100 bp
 * 4137: contig of 744 bp in length
 * 4881: contig of 100 bp
 * 4982: gap of 100 bp
 * 5014: contig of 733 bp in length
 * 5715: gap of 100 bp
 * 5815: contig of 727 bp in length
 * 6541: gap of 100 bp
 * 6641: contig of 720 bp in length
 * 7361: contig of 720 bp in length
 * 7362: gap of 100 bp
 * 7462: contig of 753 bp in length
 * 8214: gap of 100 bp
 * 8315: contig of 742 bp in length
 * 9057: gap of 100 bp
 * 9156: contig of 760 bp in length
 * 9917: gap of 100 bp
 * 10017: contig of 716 bp in length

AUTHORS Birren,B., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 11, clone RP11-126H19
 JOURNAL Unpublished
 REFERENCE

REFERENCE

AUTHORS Birren,B., Nusbaum,C., and Lander,E.
 JOURNAL Unpublished
 REFERENCE
 AUTHORS
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A.,
 Karatas,A., Kellis,C., Lander,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Maclean,C., McDonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meidrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J.J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rose,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Sevety,P.,
 Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talanais,J.,
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vasilev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

REFERENCE

REFERENCE

REFERENCE

10733	10832:	gap of 100 bp	40709	41454: contig of 746 bp in length
10833	11543:	contig of 711 bp in length	41455	41554: gap of 100 bp
11643	11543:	gap of 100 bp	41555	41512: contig of 758 bp in length
12392:	contig of 749 bp in length	42113	42412: gap of 100 bp	
12492:	gap of 100 bp	42413	43160: contig of 748 bp in length	
13224:	contig of 732 bp in length	43261	43986: contig of 736 bp in length	
13225	gap of 100 bp	43261	43986: contig of 736 bp in length	
13325	14045:	contig of 721 bp in length	43997	44056: gap of 100 bp
14046	14145:	gap of 100 bp	44097	44236: contig of 730 bp in length
14146	14894:	contig of 749 bp in length	44827	44926: gap of 100 bp
14895	14994:	gap of 100 bp	44927	45661: contig of 735 bp in length
14995	15726:	contig of 732 bp in length	45662	45761: gap of 100 bp
15727	15826:	gap of 100 bp	45762	46504: contig of 743 bp in length
15827	15862:	contig of 736 bp in length	46505	46604: gap of 100 bp
16662	16662:	gap of 100 bp	46605	46733: contig of 729 bp in length
17400:	contig of 738 bp in length	47334	47433: gap of 100 bp	
17401	17500:	gap of 100 bp	47334	47433: gap of 100 bp
17501	18229:	contig of 729 bp in length	47334	47433: gap of 100 bp
18230	18239:	gap of 100 bp	47334	47433: gap of 100 bp
18330	19041:	contig of 712 bp in length	47334	47433: gap of 100 bp
19042	19141:	gap of 100 bp	47334	47433: gap of 100 bp
19142	19860:	contig of 719 bp in length	47334	47433: gap of 100 bp
19861	19860:	gap of 100 bp	47334	47433: gap of 100 bp
19961	20680:	contig of 720 bp in length	47334	47433: gap of 100 bp
20681	20780:	gap of 100 bp	47334	47433: gap of 100 bp
20781	21508:	contig of 728 bp in length	47334	47433: gap of 100 bp
21509	21508:	gap of 100 bp	47334	47433: gap of 100 bp
21609	22316:	contig of 708 bp in length	47334	47433: gap of 100 bp
22317	22416:	gap of 100 bp	47334	47433: gap of 100 bp
22417	23158:	contig of 742 bp in length	47334	47433: gap of 100 bp
23159	23258:	gap of 100 bp	47334	47433: gap of 100 bp
23259	24028:	contig of 770 bp in length	47334	47433: gap of 100 bp
24128	24128:	gap of 100 bp	47334	47433: gap of 100 bp
24129	24867:	contig of 739 bp in length	47334	47433: gap of 100 bp
24868	24967:	gap of 100 bp	47334	47433: gap of 100 bp
24968	25695:	contig of 728 bp in length	47334	47433: gap of 100 bp
25695:	25795:	gap of 100 bp	47334	47433: gap of 100 bp
25796	25795:	contig of 723 bp in length	47334	47433: gap of 100 bp
26518	26618:	gap of 100 bp	47334	47433: gap of 100 bp
26619	26739:	contig of 741 bp in length	47334	47433: gap of 100 bp
27360	27459:	gap of 100 bp	47334	47433: gap of 100 bp
27460	28200:	contig of 741 bp in length	47334	47433: gap of 100 bp
28201	28301	gap of 100 bp	47334	47433: gap of 100 bp
29009	29109:	contig of 709 bp in length	47334	47433: gap of 100 bp
29110	29843:	gap of 100 bp	47334	47433: gap of 100 bp
29844	29843:	contig of 740 bp in length	47334	47433: gap of 100 bp
30684:	30783:	gap of 100 bp	47334	47433: gap of 100 bp
30784	31517:	contig of 734 bp in length	47334	47433: gap of 100 bp
31617:	31617:	gap of 100 bp	47334	47433: gap of 100 bp
31618	32451:	contig of 734 bp in length	47334	47433: gap of 100 bp
32352	32352:	gap of 100 bp	47334	47433: gap of 100 bp
32452	33177:	contig of 726 bp in length	47334	47433: gap of 100 bp
33178	33277:	gap of 100 bp	47334	47433: gap of 100 bp
33278	33992:	contig of 715 bp in length	47334	47433: gap of 100 bp
33993	34902:	gap of 100 bp	47334	47433: gap of 100 bp
34903	34819:	contig of 727 bp in length	47334	47433: gap of 100 bp
34820	34919:	gap of 100 bp	47334	47433: gap of 100 bp
34920	35536:	contig of 717 bp in length	47334	47433: gap of 100 bp
35536:	35736:	gap of 100 bp	47334	47433: gap of 100 bp
35737	36449:	contig of 713 bp in length	47334	47433: gap of 100 bp
36450:	36549:	gap of 100 bp	47334	47433: gap of 100 bp
36550	37290:	contig of 741 bp in length	47334	47433: gap of 100 bp
37291	37390:	gap of 100 bp	47334	47433: gap of 100 bp
37391:	38129:	contig of 739 bp in length	47334	47433: gap of 100 bp
38130	38229:	gap of 100 bp	47334	47433: gap of 100 bp
38230	38962:	contig of 733 bp in length	47334	47433: gap of 100 bp
38963	39062:	gap of 100 bp	47334	47433: gap of 100 bp
39063	39798:	contig of 736 bp in length	47334	47433: gap of 100 bp
39799	39898:	gap of 100 bp	47334	47433: gap of 100 bp
39899	40608:	contig of 710 bp in length	47334	47433: gap of 100 bp
40609	40708:	gap of 100 bp	47334	47433: gap of 100 bp
<hr/>				
Alignment Scores:				
Pred. No.:				
Score:				
Percent Similarity:				
Best Local Similarity:				
Query Match:				
DB:				
US-10-031-158-14 (1-58) x AC130306 (1-66558)				
QY	1	MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20	Length:	66558
Db	22925	ATGCAGATGTTCCCCAACGCCACATTTCCTCAATTGCTGAACAGCTCC 22984	Matches:	58
QY	21	ArgArgLeuGluHistDhrPheLeuArgAspSerLeuMetLeuLeuArgTyr 40	Conservative:	0
Db	22985	AGAAGGTGGAACTACTTCCTGCTGAAATTTCCTGCTGTTATTAAGATC 23044	Mismatches:	0
QY	41	IleGlyIleValBargArgGalaThrArgPheTrpProArgArgYThrPro 58	Indels:	0
Db	23045	ATGGCAAGAAAGAGCACACGATTCTGGATTCAGGAGGACACACCA 23098	Gaps:	0
RESULT 25				
AF159056	AF159056	A Homo sapiens T-cell gamma receptor locus, complete sequence.	PRI 17-AUG-2001	
LOCUS	AF159056	140691 bp	DNA	linear
DEFINITION				
ACCESSION	AF159056			
VERSION	AF159056.1			
KEYWORDS				

	repeat_region	/note="v6P"	AC006033/c	171816 bp DNA linear PRI 31-JAN-2004
	/pseudo		LOCUS	Homo sapiens BAC clone RP11-121A8 from 7, complete sequence.
	/repeat_element(78838..79000)		DEFINITION	
	/rpt_family="MIR"		ACCESSION	AC006033
	/rpt_type=dispersed		VERSION	AC006033.2 GI:4309948
	/repeat_element(80629..81096)		KEYWORD	HTG.
V_segment	/rpt_type=dispersed		SOURCE	Homo sapiens (human)
	/notes="V4P"		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	/pseudo		AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
	/repeat_element(82330..83651)		REFERENCE	1 (bases 1 to 171816)
	/rpt_family="LTRII"		AUTHORS	Wagner-McPherson,C., Layman,D., Maas,J., Jaeger,S., Walker,R.,
	/rpt_type=dispersed		REFERENCE	Wylie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.E.,
	/repeat_element(82876..83159)		AUTHORS	Fewell,G.A., Delehaunty,K.D., Miner,T.J., Nash,W.B., Cordes,M.,
	/rpt_family="Alu"		REFERENCE	Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S.,
	/rpt_type=dispersed		AIAK,A., Vanbrunt,A., Nguyen,C., Du,F., Lamar,B., Courtney,L.,	
	/repeat_element(85826..86088)		REFERENCE	Kalicki,J., Ozarsky,P., Bielicki,L., Scott,K., Holmes,A.,
	/rpt_family="MER2"		AUTHORS	Harkins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C.,
	/rpt_type=dispersed		REFERENCE	Dauphin-Kohlb erg,S., Kozlowski-Reilly,A., Leonard,S., Rohlfing,T.,
	86291..86368		AUTHORS	Rock,S.M., Tim-Wallace,A.M., Abbott,A., Minx,J., Maupin,R.,
	/rpt_family="MIR"		REFERENCE	Stromatt,C., Latreille,P., Miller,N., Johnson,D., Murray,J.,
	/rpt_type=dispersed		AUTHORS	Woesner,J.P., Wendt,M.C., Yang,S.P., Schultz,B.R., Wallis,J.W.,
	86542..86531		REFERENCE	Spieth,J., Bieri,T.A., Nelson,J.O., Wohldmann,P.E.,
	/rpt_family="MERS"		AUTHORS	Cook,L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,J.A.,
	/rpt_type=dispersed		REFERENCE	Mardis,E.R., Clifton,S.W., Chissoe,S.L., Marra,M.A., Raymond,C.,
	/repeat_element(90148..90424)		AUTHORS	Hauen,E., Gillett,W., Zhou,Y., James,R., Phelps,K., Iandolo,S.,
	/rpt_family="Alu"		REFERENCE	Bubb,K., Simms,E., Levy,R., Clendenning,J., Kaul,R., Kent,W.J.,
	/rpt_type=dispersed		AUTHORS	Furey,T.S., Baertsch,R.A., Brent,M.R., Keibler,E., Fluke,P.,
	97655..97996		REFERENCE	Bork,P., Suyama,M., Bailey,J.A., Portnoy,M.E., Torrents,D.,
	/note="JP1"		AUTHORS	Chinwalla,A.T., Gish,W.R., Eddy,S.R., McPherson,J.D., Olson,M.V.,
	/repeat_element(9475..99769)		REFERENCE	Eichler,E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.
	/rpt_type=dispersed		AUTHORS	The DNA Sequence of human chromosome 7
	100267..100327		REFERENCE	Nature 424 (6945), 157-164 (2003)
	/note="JP"		REFERENCE	22757994
J_segment	/repeat_element(103808..104065)		REFERENCE	2 (bases 1 to 171816)
	/rpt_family="Alu"		AUTHORS	Arnett,C., Le,T.P. and Wohldmann,P.
	/rpt_type=dispersed		REFERENCE	The Sequence of Homo sapiens BAC Clone RP11-121A8
	104364..104423		AUTHORS	Unpublished (2001)
	/note="J1"		REFERENCE	3 (bases 1 to 171816)
	107293..107592		AUTHORS	Waterson,R.H.
	/rpt_family="Alu"		REFERENCE	Direct Submission
	/rpt_type=dispersed		AUTHORS	Submitted (27-FEB-1999) Department of Genetics, Washington
	108009..108085		REFERENCE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
	/rpt_family="MIR"		AUTHORS	MO 63108, USA
	/rpt_type=dispersed		REFERENCE	4 (bases 1 to 171816)
	108237..108566		AUTHORS	Waterson,R.
	/note="C1 exon 1"		REFERENCE	Direct Submission
			AUTHORS	Submitted (27-FEB-1999) Department of Genetics, Washington
			REFERENCE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
			AUTHORS	5 (bases 1 to 171816)
			REFERENCE	Waterson,R.
			AUTHORS	Direct Submission
			REFERENCE	Submitted (21-DEC-1999) Department of Genetics, Washington
			AUTHORS	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
			REFERENCE	6 (bases 1 to 171816)
			AUTHORS	Waterson,R.
			REFERENCE	Direct Submission
			AUTHORS	Submitted (29-APR-2003) Department of Genetics, Washington
			REFERENCE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
			AUTHORS	7 (bases 1 to 171816)
			REFERENCE	Wilson,R.
			TITLE	Direct Submission
			COMMENT	Submitted (31-JAN-2004) Department of Genetics, Washington
			COMMENT	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
			COMMENT	On Mar 1, 1999 this sequence version replaced gi:3907471.
			COMMENT	----- Genome Center
			COMMENT	Center: Washington University Genome Sequencing Center
			COMMENT	Center code: WUGSC
			COMMENT	Web site: http://genome.wustl.edu
			COMMENT	Contact: sapiens@watson.wustl.edu

Center project name: H_NH0121A08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between each clone, i.e. a subjunction.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., paired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NRGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see
<http://www.hrgri.nih.gov/DLR/J3TB/CHR7>, send
mailto:egreen@nrgri.nih.gov, or see <http://genome.wustl.edu>

The RPCL-III human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tattone, M., Cataneo, J.J. and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-21A8
actual end is at 171816 of RP11-21A8.
[Inquire](#) [Print](#)

```

repeat_region 3941..3976 /RPT_family="AT-rich"
repeat_region 4114..4171 /RPT_family="MIR"
repeat_region 4175..4305 /RPT_family="MER1-type"
repeat_region 4623..4781 /RPT_family="MER2-type"
repeat_region 4889..5191 /RPT_family="L2"
repeat_region 5209..5499 /RPT_family="MaLR"
repeat_region 5512..5623 /RPT_family="(TA)n"
repeat_region 7420..7746 /RPT_family="MER2-type"
repeat_region 8188..8258

US-10-031-158-14 (1-58) x AC006033 (1-171816)
QY          1 MetGlnMetPheProProSerProLeuPheIleGlnIleLeuLeuIysGlnSerSer 20
Db          86565 ATGCAGATGTTCCCAAGCCAACTTATTCCTCAAATGCTGAACAGAGCTCC 86506
QY          21 ArgGluGluGluIstSerPheAlaPhleuIgAsnPheSerIeuMetLeuLauArgTyr 40
Db          86505 AGAAGCTGTGACATACCTTGCTCTGAGAAATTTCCTGTATGTTATTAGATA 86446

```

QY	41	IleGlyLysArgArgAlaThrArgPheTrpAspProArgGlyThr-Pro	58
Db	86445	ATTGCCAAGAAAGAGACACGATCTGGATCCCAAGGGAAACCCA	86392
RESULT	27		
HSTCELG1			
DEFINITION		Human gene fragment for T-cell receptor gamma 1 chain constant region (loc. on chromosome 7p15).	
LOCUS		HSTCELG1	
REFERENCE	1		
AUTHORS	Schlegel,R., Endege,W.O. and Monahan,J.B.		
TITLE	Genes differentially expressed in human prostate cancer and their use		
JOURNAL	Patent: WO 016060-A 25002 23-AUG-2001; Millennium Predictive Medicine, Inc. (US)		
FEATURES	source		
	1. .486 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
ORGANISM	Homo sapiens (human)		
ORIGIN			
source			
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Murie,C., Waldman,R.A., Morton,C.C., Bongiovanni,K.F., Waldman,T.A., Shows,T.B. and Seidman,J.G.		
TITLE	Human gamma-chain genes are rearranged in leukaemic T cells and map to the short arm of chromosome 7		
JOURNAL	Nature 316 (6028), 549-552 (1985)		
MEDLINE	85296267		
PUBMED	3875797		
FEATURES			
	Location/Qualifiers		
	1. .400		
	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
CDS			
	<1..27. <28..>357 /note="put. intron" /note="unnamed protein product; (g1) C region fragment (357 is 1st base in codon)"		
	/codon_start=3 /protein_id="P0AE82035.1" /db_xref="GI:3863935" /translation="KQLDADVSVPRPTIPLPSIAETKLKLAGTYCLIEKKFPDVKIH WEEKKNTLGSQBGNMKNDTMKPSMLTVPEKSLDKERCIVRHENKNQVDQT IFPPKT"		
intron			
ORIGIN			
source			
	Alignment Scores: Pred. No.: 8.44e-30 Score: 304.00 Percent Similarity: 100.00% Best Local Similarity: 98.28% Query Match: 99.02%	Length: 400 Matches: 57 Conservative: 1 Mismatches: 0 Indels: 0 Gaps: 0	
Alignment Scores:			
Pred. No.:	8.44e-30	Length:	400
Score:	304.00	Matches:	57
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.28%	Mismatches:	0
Query Match:	99.02%	Indels:	0
DB			
US-10-031-158-14 (1-58) x CQ493135 (1-486)			
QY	1	MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer	20
Db	411	ATGGAGATCTTCCCCAACCCACTATTTCCTCTTCAATTGTGAACAAAGTC	352
QY	21	ArgArgLeuGluHisthRpheLeuArgAsnPheSerLeuMetLeuLeuArgTyr	40
Db	351	AGAGGCTGGACATACTTGTCTCTGAAAMTTTCCCTGATGTATAAGATC	292
QY	41	IleGlyLysArgArgAlaThrArgPheTrpAspProArgGlyThr-Pro	58
Db	291	ATTGCCAAGAAAGAGAGAACCGATTCTGGATCCCAAGGGAAACCCA	238
RESULT	29		
CQ144550			
LOCUS	CQ144550		
DEFINITION	Sequence 14572 from Patent WO0157276.		
VERSION	CQ144550.1		
SOURCE			
KEYWORDS			
ORGANISM	Homo sapiens (human)		
ORIGIN			
source			
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.		
TITLE	Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow		
JOURNAL	Patent: WO 0157276-A 14572 09-AUG-2001; Academic, Inc. (US)		
FEATURES	Location/Qualifiers		
	1..316		
source			
	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
ALIGNMENT			
QY	21	ArgArgLeuGluHisthRpheLeuArgAsnPheSerLeuMetLeuLeuArgTyr	40
Db	100	AGAACGCTGGACATACCTTGCTCTTGAGAAATTTCCTGAGTTATAGATC	159
QY	41	IleGlyLysArgArgAlaThrArgPheTrpAspProArgGlyThr-Pro	58
Db	160	ATTGCCAAGAAAGAGAGAACCGATTCTGGATCCCAAGGGAAACCCA	213
ORIGIN			
source			
	Alignment Scores: Pred. No.: 1.17e-29 Score: 302.00 Percent Similarity: 100.00% Best Local Similarity: 100.00%	Length: 316 Matches: 57 Conservative: 0 Mismatches: 0	
RESULT	28		
CQ493135/C			
LOCUS	CQ493135		
DEFINITION	Sequence 25002 from Patent WO0160860.		
VERSION	CQ493135.1		
ORIGIN			
source			
	Alignment Scores: Pred. No.: 1.17e-29 Score: 302.00 Percent Similarity: 100.00% Best Local Similarity: 100.00%	Length: 316 Matches: 57 Conservative: 0 Mismatches: 0	

Query Match: 98.37% Indels: 0
DB: 6 Gaps: 0

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

AUTHORS 2 Human genome-derived single exon nucleic acid probes useful for TITLE analysis of gene expression in human lung

JOURNAL Patent: WO 018603-A 14092 15-Nov-2001;

Db Aeomica, Inc. (US) Location/Qualifiers

FEATURES source

RESULT 30 1. .316 /organism="Homo sapiens"

CQ204403 /mol_type="unassigned DNA"

DEFINITION /db_xref="taxon:9606"

LOCUS 316 bp DNA linear PAT 21-JAN-2004

SEQUENCE Sequence 6680 from Patent WO0157271.

ACCESSION CQ204403

VERSION CQ204403.1 GI:41190250

REFERENCE 1

AUTHORS 2 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

JOURNAL Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human breast and bt 474 cells

PATENT: WO 0157271-A 6680 09-AUG-2001; Asomics, Inc. (US) Location/Qualifiers

FEATURES 1. .316

Source /organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AF159056.1~EXPRESSED IN BT474, SIGNAL = 1.3-SWISSPROT HIT: P03886; EVALU 7.00e-58 NT HIT: MI4396.1; EVALU 0.00e+00-EST HUMAN HIT: BR679123.1, EVALU 0.00e+00"

ORIGIN

Alignment Scores:

Pred. No.: 1.17e-29 Length: 316

Score: 302.00 Matches: 57

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.37% Indels: 0 Gaps: 6

DB: US-10-031-158-14 (1-58) x CQ302987 (1-316)

QY 2 GluMetPheProProSerProLeuPheLeuGlnIleLeuIlyGlnSerSerArg 21

Db 2 CAGATGTTCCCAAGGCCACTATTTCCTCTCAATTGTGAAACAAGCTCCAGA 61

QY 22 ArgLeuGluHisThrPheValPheLeuArgIleSerIleLeuIleLeuArgTyrIle 41

Db 62 AGCTGGACATACCTGCTCTGAGAAATTCCCTGAGTATTAGATCATT 121

QY 42 GlyLysIysArgGalaIthArgPheTrpAspProArgGlyIlyPro 58

Db 122 GCGCAAGAAAGAGGAGAACGATCTGGATCCCGAGGGACACCA 172

RESULT 31

CQ302987 Alignment Scores:

LOCUS Pred. No.: 7.4e-29 Length: 569

DEFINITION Score: 298.00 Matches: 57

ACCESSION Percent Similarity: 98.28% Conservative: 0

VERSION Best Local Similarity: 98.28% Mismatches: 1

ORIGIN

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

REFERENCE 1 Schlegel, R., Endge, W.O. and Monahan, J.E.

AUTHORS 2 Genes differentially expressed in human prostate cancer and their use

JOURNAL Patent: WO 0160860-A 43494 23-AUG-2001;

Db Millennium Predictive Medicine, Inc. (US) Location/Qualifiers

FEATURES 1. .569

Source /organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match: 97.07% Indels: 0 Gaps: 0

DB: 6

US-10-031-158-14 (1-58) x CQ511627 (1-569)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20

Db 460 ATTCAGATGTTCCCAAGCCACATTCTTCAATGCTGAAACAAGCTC 401

Qy 21 ArgArgLeuGlnIleThrPheLeuGlnAsnPheSerLeuMetLeuLeuArgTyr 40

Db 400 AGAACGCTGACATACCTTGCTCTGAGAATTTCGGATGTTAGATCC 341

Qy 41 IleGlyLysValSargArgAlaThrArgPheTrpAspProArgGlyGlyThrPro 58

Db 340 ATTGCCAAGAAAGAGCACACGATCTGGATCCCGAGGGAAACCCA 287

RESULT 33

HUMTCGCG HUMTCGCG

LOCUS Human T-cell receptor germline gamma-chain (TCRG2) gene C2-region 330 bp DNA linear PRI 13-JAN-1995

DEFINITION allele gamma-2b, exon 1.

ACCESSION M15002

VERSION M15002.1 GI:339083

KEYWORDS C-region; T cell receptor gamma-chain; T-cell receptor; germline.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Lefranc, M.P., Forster, A., and Rabbits, T.H.

AUTHORS Genetic polymorphism and exon changes of the constant regions of the human T-cell rearranging gene gamma

TITLE proc. Natl. Acad. Sci. U.S.A. 83 (24), 9596-9600 (1986)

JOURNAL MEDLINE 87092294

PUBMED 2879283

COMMENT Original source text: Human B-cell prolymphocytic leukemia line D-PBL DNA, clone Lambda-D7. Entry revisions for [1] kindly provided by M.-P. Lefranc, 22-JUN-1988.

FEATURES SOURCE

1. (bases 1 to 330) Location/Qualifiers

2. .330 /organism="Homo sapiens"

3. /mol_type="genomic DNA"

4. /db_xref="taxon:9606"

5. /map="p15-p14"

gene

1. .330 /gene="TCRG2"

1. .330 /gene="TCRG2"

exon

1. .330 /note="G00-120-409"

/number=1

ORIGIN 165 bp upstream of BamHI site.

Alignment Scores:

Pred. No.: 1.32e-28 Length: 330

Score: 294.28% Matches: 55

Percent Similarity: 98.28% Conservative: 2

Best Local Similarity: 94.83%

Query Match: 95.77%

DB: 9

Db: 0 Gaps: 0

US-10-031-158-14 (1-58) x HUMTCGCG (1-330)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20

Db 13 ATTCAGATGTTCCCAAGCCACATTCTTCAATGCTGAAACAAGCTC 72

Qy 21 ArgArgLeuGlnIleThrPheLeuGlnAsnPheSerLeuMetLeuLeuArgTyr 40

Db 73 AGAACGCTGACATACCTTGCTCTGAGAATTTCGGATGTTAGATCC 132

Qy 41 IleGlyLysValSargArgAlaThrArgPheTrpAspProArgGlyGlyThrPro 58

Db 296173

Db 1.33 ATTGGCAAGAAAGAGCAACAGATCTGGATCCCGAGGGAGACACCA 186

RESULT 34

HSTRGC54 HSTRGC54

LOCUS Human truncated mRNA from TRG gamma gene V(g)8-J(g)P2-C(g)2 with nonproductive V-J arrangement.

DEFINITION X06776

ACCESSION X06776.1 GI:37343

VERSION X06776.1

KEYWORDS constant region; Joining region; T-cell receptor; T-cell receptor gamma, variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Tighe, L., Forster, A., Clark, D.M., Boyleston, A.W., Lavenir, I. and Rabbits, T.H.

AUTHORS Unusual forms of T cell gamma mRNA in a human T cell leukemia cell line: implications for gamma gene expression

JOURNAL Eur. J. Immunol. 17 (12), 1729-1736 (1987)

MEDLINE 88083067

PUBMED 296173

COMMENT M017 TRG gamma allele 1 derived productive cDNA. see x06775 for further allele 2 nonproductive cDNA; see x06774 for location/Qualifiers

FEATURES SOURCE

1. .635 /organism="Homo sapiens"

2. .217 /mol_type="mRNA"

3. /db_xref="taxon:9606", /clone="M7C54"

4. /cell_lines="M017"

CDS /clone_lib="Lambda gt10"

5. /codon_start=1 /protein_id="CAA29944.1"

6. /db_xref="GI:1335357", /translation="LVENAYATHWILHQEGKAPQRQLYDYSNRSVWLESQISREKVHNYASPGKSLKPFILENLIERDPSGVYCA"

7. /note="unnamed protein product; Protein sequence is in conflict with the conceptual translation; V(g)8 region (AA 1-72)"

8. /codon_start=1 /protein_id="CAA29944.1"

9. /db_xref="GI:1335358", /translation="PRWIKPAFKGTRLIVSPDKOLDADVSPKPPTFLPSIAETKQKAGTYCLLEKEFPDPDKIHNOEKSVTIGSQEGNIMKNDYMKPSWLTVPEESLDKEHRCTYRHENNKNGIDQEIFFPPKIVUMCHIKKK"

misc_feature 10. /note="J(g)P2 region (truncated at 5' end)"

misc_feature 11. /note="C(g)2 (exon 1)"

misc_feature 12. /note="C(g)2 (exon 1)"

misc_feature 13. /note="pot. polyA signal"

misc_feature 14. /note="pot. polyA signal"

misc_feature 15. /note="translated intron + polyA sequence"

ORIGIN Alignment Scores:

Pred. No.: 2.73e-28 Length: 635

Score: 294.00 Matches: 55

Percent Similarity: 98.28% Conservative: 2

Best Local Similarity: 94.83%

Mismatches: 1

Query Match:	95.77%	Indels:	0
DB:	9	Gaps:	0
QY	1 MetGlnMetpheProProSerProLysPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20	misc_feature	EKS" 43. .91 /note="Jg2 region"
Db	289 ATGCAAGATGTTCCCTCAAGGCCACTAATTTCTTCATGTGAAACAAACTCC 348	misc_feature	92. .705 /note="Cg2 region"
Qy	21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40	misc_feature	421. .422 /note="exon/exon boundary" 469. .470 /note="exon/exon boundary"
Db	349 AGAACGCTGGACATACCTTGCTCTCTTGAGAAATTTCAGATATTAGATA 408	misc_feature	517. .518 /note="exon/exon boundary" 565. .566 /note="exon/exon boundary"
QY	41 IleGlyLysIvaBargArgAlaThrArgPhePhePheAspProArgArgYThPro 58	ORIGIN	
Db	409 ATTGGCAGAAGAGAGCACACGATCTGGATCCAGGGGACACCA 462	Alignment Scores:	
RESULT 35	HSTRGC10	Pred. No.:	3.14e-28
LOCUS	HSTRGC10	Score:	294.00
DEFINITION	Human aberrant mRNA from TRG gamma gene with unrearranged J(g)2	Percent Similarity:	98.28%
ORGANISM	Homo sapiens	Best Local Similarity:	94.83%
ACCESSION	X06775	Query Match:	95.77%
KEYWORDS	constant region; joining region; T-cell receptor; T-cell receptor gamma.	DB:	9
SOURCE	Homo sapiens (human)	Length:	720
ORGANISM	Homo sapiens	Matches:	55
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 720)	Conservative:	2
AUTHORS	Tiche,L., Porter,A., Clark,D.M., Boylston,A.W., Laverin,I. and Rabbits,T.H.	Mismatches:	1
TITLE	Unusual forms of T cell gamma mRNA in a human T cell leukemia cell line: implications for gamma gene expression	Indels:	0
JOURNAL	Eur. J. Immunol. 17 (12), 1729-1736 (1987)	Gaps:	0
MEDLINE	88083067	US-10-031-158-14 (1-58) x HSTRGC10 (1-720)	
COMMENT	PM17c10 cDNA is derived from TRG gamma locus allele 2; see x06776 for further allele 2 derived nonproductive cDNA; See x06774 for MOLM17 cDNA representing productive TRG gamma rearrangement of allele 1	QY	1 MetGlnMetPheProProSerProLysPhePhePheLeuGlnLeuLeuGlnSerSer 20
PUBMED	2961573	Db	104 ATCCAGATGTTCCCCAACGCCACATTTCCTTCATTCGAACAAACTCC 163
FEATURES	source	QY	21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
CDS	1. .720 /organisms="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="pm17c10" /cell_line="MOLM17" /clone_lib="lambda gt10" 1. .42 .42 unnamed protein product; Protein sequence is in conflict with the conceptual translation; open frame with J(g)2" /codon_start=1 /protein_id="CAA29942.1" /db_xref="GI:1335255" /translaton="GNELBEFLIWTESLW" 14. .22 /note="nanomer recombination signal" 35. .41 /note="heptamer recombination signal"	Db	164 AGAGGCTGAACATACCTTGCTCTGAGAAATTTCAGATATTAGATA 223
CDSD		QY	41 IleGlyLysIvaBargArgAlaThrArgPhePhePheAspProArgArgYThPro 58
misc_feature		Db	224 ATTGGCAGAAGAGAGCACACGATCTGGATCCAGGGACACCA 277
misc_feature		RESULT 36	
FEATURES	source	HUMTRGAA	HUMTRGAA
CDS		LOCUS	1013 bp
CDSD		DEFINITION	mRNA, 1 linear PRI 14-JAN-1995
misc_feature		ORGANISM	Homo sapiens (clone HGPO8) T cell receptor gamma-chain mRNA, C2 region.
misc_feature		ACCESSION	M27331
misc_feature		VERSION	M27331.1 GI:1540458
misc_feature		KEYWORDS	T cell receptor gamma-chain; constant region.
misc_feature		SOURCE	Homo sapiens (human)
misc_feature		ORGANISM	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1013)
JOURNAL		JOURNAL	Yosikai,Y., Toyonaga,B., Koga,Y., Kimura,N., Grieser,H. and Mak,T.W.
MEDLINE		COMMENT	Reportoire of the human T cell gamma genes: high frequency of nonfunctional transcripts in thymus and mature T cells
PUBMED		COMMENT	Eur. J. Immunol. 17 (1), 119-126 (1987)
COMMENT		COMMENT	87133835
FEATURES	source	294984	On Sep 21, 1994 this sequence version replaced gi:341669.
CDSD		gene	Original source text: Homo sapiens PHA-stimulated peripheral T cell cDNA to mRNA.
misc_feature		Location/Qualifiers	
misc_feature		1. .1013	
misc_feature		/organisms="Homo sapiens"	
misc_feature		/mol_type="mRNA"	
misc_feature		/db_xref="taxon:9606"	
misc_feature		/map="7p15-p14"	
misc_feature		/clone="HGPO8"	
misc_feature		/tissue_type="PHA-stimulated peripheral T cell"	
misc_feature		1. .1013	
misc_feature		/gent="TCRGCC2"	
misc_feature		<1. .570	
misc_feature		/gen="TCRGCC2"	
misc_feature		/note="This CDS feature is included to show the	

TITLE		JOURNAL Science 237 (4810), 64-67 (1987)
JOURNAL		MEDLINE
MEDLINE		PUBMED
PUBMED		295517
COMMENT		Original source text: Human (cell line IDP2), cDNA to mRNA, clone IDP2.11.
FEATURES	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
SOURCE	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
mRNA	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
gene	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
CDS	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
FEATURES	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
source	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ORGANISM	Homo sapiens (human)	
REFERENCE	Sequence 3344 from Patent WO0194629.	
ACCESSION	AX332835	
VERSION	AX332835.1 GI:18123469	
KEYWORDS	.	
FEATURES	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
source	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ORGANISM	Bukarvota; Metzaoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horriean, S., Soppe, D.R., and Wever, Z.	
AUTHORS	Cancer gene determination and therapeutic screening using signature gene sets	
JOURNAL	Patent: WO 0194629-A 3344 13-DEC-2001; Avalon Pharmaceuticals (US)	
FEATURES	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
source	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ORIGIN	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ALIGNMENT	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
SCORE	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ALIGNMENT	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
Scores:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
Pred. No.:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
Score:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
Percent Similarity:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
Best Local Similarity:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
Query Match:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
DB:	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
US-10-031-158-14 (1-58) x AX332835 (1-1421)	US-10-031-158-14 (1-58) x AX332835 (1-1421)	
QY	1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20	
Db	423 ATGCAGATGTTCCCCAACCCACTTTCCTCTCAATTGGAAACAAACTCC 482	
QY	21 ArgArgLeuGlnIleThrPheValPheLeuArgAsnHeSerLeuMetLeuIeuAspTyr 40	
Db	483 AGAGGCTGGACATACTACCTTGCTCTTGAGAAATTTCAGATATTATAAGATAC 542	
QY	41 IleGlyLysArgArgAlaThrArgPhePhePheProArgArgGlyThrPro 58	
Db	543 ATTGCGAAGAAAGAGCACGATTCGGATCCACAGGGACACCA 596	
RESULT	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
HUMTCGXH	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
DEFINITION	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
LOCUS	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ACCESSION	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
VERSION	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
KEYWORDS	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
SOURCE	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
ORGANISM	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
REFERENCE	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
AUTHORS	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
TITLE	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
JOURNAL	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	
PUBLISHED	STRUCTURALLY DIVERGENT HUMAN T CELL RECEPTOR GAMMA PROTEINS ENCODED BY DISTINCT GAMMA GENES	

COMMENT Original source text: Human T-cell line HPA-MLT, cDNA to mRNA, clones pT-gamma-[1, 2]. Computer-readable sequence of [1] kindly provided by D.P.Dialymas, 31-OCT-1986.

An aberrant rearrangement at the V-J junction causes a frame shift that leads to peptide termination at the 'taa' codon at positions 370-372.

A polyadenylation signal can be found at positions 1400 to 1405.

FEATURES Source Location/Qualifiers

CDS 1. 1-1421 /organism="Homo sapiens"
 /mol type="mRNA"
 /db_xref="taxon:9606"
 4. 979 /note="pseudo-TCG pept"
 /pseudo
 /codon_start=1
 4. 63 /note="pseudo-TCG signal pept"
 /pseudo
 mat_peptide 64. 976 /note="pseudo-TCG mature pept"
 /pseudo

ORIGIN 16 bp upstream of ApaI site; chromosome 7.

Alignment Scores:

Pred. No.:	6.72e-28	Length:	1421
Score:	294.00	Matches:	55
Percent Similarity:	98.28%	Conservative:	2
Best Local Similarity:	94.83%	Mismatches:	1
Query Match:	95.77%	Indels:	0
DB:	9	Gaps:	0

US-10-031-158-14 (1-58) x HUMTGXH (1-1421)

QY 1 Met Glu Met Phe Pro Pro Ser Pro Leu Gln Ile Leu Lys Gln Ser 20
 Db 423 Arg CAG AGAT GTT TCC CCA AGGCC ACT ATTT TTCT CCT CA ATT GCT GAA AAC AA ACT CC 482
 QY 21 Arg Arg Leu Glu Ile His Thr Phe Val Phe Leu Ile Arg Asp Ser Ser Leu Met Leu Leu Arg Tyr 40
 Db 483 AGA AGC GGT GG A GAC ATAC TT CTG CTG TT GAA ATT TT CC A GAT ATT ATT ATT A GAT AC 542
 QY 41 Ile Gly Ile Val Sarg Arg Gln Ile Thr Arg Phe Pro Asp Pro Arg Arg Gly Ile Thr Pro 58
 Db 543 ATGG CAG A GAG A GAG A GCA CAC GAT CCT CGG AT CCC CAG GGG GAA CAC CCA 596

Search completed: December 8, 2004, 08:54:17
 Job time : 1916 secs

THIS PAGE BLANK (USPTO)

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2004, 06:09:26 ; Search time 247 Seconds
(Without alignments)
1232.658 Million cell updates/sec

Title: US-10-031-158-14

Perfect score: 307

Sequence: 1 MQMFPPSPPLFFFLQLLKQSS.....RYIGKKRATRFWDPRRGTP 58

Scoring table: BLOSUM62

	Xgapop	Xgapext	Ygapext	Fgapop	Fgapext	Delop	Delext
C	10.0	0.5	0.5	6.0	7.0	6.0	7.0
C	22	298	97.1	569	5	ABV2593	
C	23	294	95.8	1560	10	ABL65007	
C	24	294	95.8	1560	10	ABK64987	
C	25	294	95.8	1799	6	ABZ25381	
C	26	290	94.5	1080	2	AHQ3617	
C	27	290	94.5	1060	12	ADP0049	
C	28	284	92.5	1046	12	ADP0049	
C	29	284	92.5	1080	1	AAN91629	
C	30	279	90.9	1080	1	AAN91629	
C	31	259	84.4	533	5	ABV37856	
C	32	251	81.8	460	3	AAQ04015	
C	33	245	79.8	1155	3	AAQ3617	
C	34	240	78.2	1022	5	ABV2593	
C	35	240	78.2	1022	5	ABV24072	
C	36	240	78.2	1022	5	ABV24072	
C	37	240	78.2	1022	5	ABV25823	
C	38	240	78.2	1022	5	ABV24034	
C	39	240	78.2	1022	5	ABV23986	
C	40	240	78.2	1022	5	ABV23991	
C	41	240	78.2	1022	5	ABV24108	
C	42	240	78.2	1022	5	ABV23814	
C	43	240	78.2	1022	5	ABV25918	
C	44	240	78.2	1022	5	ABV25974	
C	45	240	78.2	1022	5	ABV29953	

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_2n.model -DEV=x1h
-O=/cgn2_1/USP0/spool/US10031158/runat_06122004_082659_15877/app_query.fasta_1.199
-DBN=GenSeq 23Sep04 -QFM=fasta -SUFFIX=xmg -MINMATCH=0.1 -LOCPCL=0
-LOOKEXT0 -UNITS=bits -START=-1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cai
-LIST=45 -DOCAALIGN=200 -TTR SCORE=pc -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORMSCORE=0 -HEAPSIZE=500 -MINLEN=200000000
-USER=US10031158 @CGN 1 1-352 @runat_06122004_082659_15877 -NCPU=6 -ICPU=3
-NOMAP -LARGEQUERY -NEG3 SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : N_GenSeq 23Sep04:*

- 1: geneseqn190s:*
- 2: geneseqn190s:*
- 3: geneseqn200s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	307	100.0	426	AAC00681 Human sec
2	307	100.0	470	Aak2682 Human bon
3	307	100.0	470	Abs01569 Human gen
4	307	100.0	477	Aba43588 Human bre
5	307	100.0	477	Aak27758 Human bon
6	307	100.0	477	Abs02210 Human gen

RESULT 1

ID	Description
AAC00681	AAC00681 Standard; cDNA; 426 BP.
XX	
AC	AAC00681;
XX	
DT	06-OCT-2000 (first entry)
XX	
DB	Human secreted protein 5' EST, SEQ ID NO: 679.
XX	
KW	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
XX	
OS	Homo sapiens.
XX	
BN	EP1033401-A2.
XX	
PD	06-SEP-2000.
XX	
PP	21-FEB-2000; 2000EP-00200610.
XX	
PR	26-FEB-1999; 99US-0122487P.
XX	
PA	(GEST) GENSET.
XX	
DI	Dumas Milne Edwards J, Ducleart A, Giordano J;
XX	
DR	WPI; 2000-500381/45.
XX	
DR	P-PSDB; AAC00675.

ALIGNMENTS

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNA that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 1; SEQ ID NO 679; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. An ORF has been identified within the
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
 CC derived from 30 different tissues. EST sequences usually correspond
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
 CC well suited for isolating cDNA sequences derived from the 5' ends of
 CC mRNAs and even in those cases where longer cDNA sequences have been
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length
 CC cDNAs and genomic DNA. 5' ESTs are also used in diagnostic, forensic,
 CC gene therapy and chromosome mapping procedures. They are used to obtain
 CC upstream regulatory sequences and to design expression and secretion
 CC vectors.
 XX
 SQ Sequence 426 BP; 151 A; 83 C; 88 G; 104 T; 0 U; 0 Other;
 Alignment Scores:
 pred. No.: 4.87e-34
 Score: 307.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 3
 Gaps: 0

US-10-031-158-14 (1-58) x AAC00681 (1-426)

Qy 1 MetGlnMetPheProProSerProLeuIlePhePhePheLeuGlnLeuLeuLysGlnSer 20
 Db 94 ATGCAGATGTTGCCAGCCACTATTTCTTCCTCAATTGCTGAACAAAGTCC 153

Qy 21 ArgArgLeuGluIleIlePheValPheLeuGlnPheSerLeuMetLeuLeuArgTyr 40
 Db 154 AGAGGGCTGAACTACCTTGCTCTGAGAAATTTCCTGAGTTTAAGATAC 213

Qy 41 IleGlyLysValSArgArgPheIleArgPheTrpAspProArgArgGlyThrPro 58
 Db 214 ATTGCGAAGAAGAACGAACTGGATCCAGGAGGGACACCA 267

RESULT 2

AAC26982

ID AAC26982 standard; DNA; 470 BP.

XX
 AC AAC26982;
 XX
 DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 1539.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; SB.

OS Homo sapiens.

XX WO200157276-A2.

XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-023467P.

PR 21-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 1539; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention.

XX Sequence 470 BP; 148 A; 102 C; 87 G; 133 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5.56e-34 Length: 470
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4
 Gaps: 0

US-10-031-158-14 (1-58) x AAC26982 (1-470)

Qy 1 MetGlnMetPheProProSerProLeuIlePhePhePheLeuGlnLeuLeuLysGlnSer 20
 Db 203 ATGCAGATGTTGCCAGCCACTATTTCTTCCTCAATTGCTGAACAAAGTCC 262

Qy 21 ArgArgLeuGluIleIlePheValPheLeuGlnPheSerLeuMetLeuLeuArgTyr 40
 Db 263 AGAGGGCTGAACTACCTTGCTCTGAGAAATTTCCTGAGTTTAAGATAC 322

Qy 41 IleGlyLysValSArgArgPheIleArgPheTrpAspProArgArgGlyThrPro 58
 Db 323 ATTGCGAAGAAGAACGAACTGGATCCAGGAGGGACACCA 376

RESULT 3

ABS01569

ID ABS01569 standard; DNA; 470 BP.

XX
 AC ABS01569;
 XX
 DT 19-AUG-2002 (first entry)

XX Human genome-derived single exon probe from lung SEQ ID NO 1560.

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome; pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia; primary ciliary dyskinesia; pulmonary hypertension; hyaline membrane disease.

XX Homo sapiens.

XX WO200186003-A2.

XX
 PR 15-NOV-2001.

XX
 PF 30-JAN-2001; 2001WO-US000665.

XX
 PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00609408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PT
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.

XX PS
 Claim 1; SEQ ID NO 1560; 634pp; English.

CC The invention relates to a spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

CC Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

CC The invention relates to a spatially-addressable set of single exon nucleic acid probes, having one of complements or the 12387 open reading frames derived from the 1614 probes. Also included are a microarray comprising the novel set of probes which hybridize at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array, identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary hamosiderosis, pulmonary histiocytosis, lymphangioleiomoytosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 470-BP; 148 A; 102 C; 87 G; 133 T; 0 U; 0 Other; SQ Alignment Scores:
 Pred. No.: 5 5.56e-34 Length: 470
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 6 Indels: 0
 Gaps: 0

XX US-10-031-158-14 (1-58) X ABS01569 (1-470)

Oy 1 MetGluMetPheProProSerProLeuPhePhePheLeuGlnIleLeuLeuLysGlnSerSer 20
 Db 203 ATTCAGATGTTCGCCCAAGCCACTATTCTTCCCTCAATGCTGAACAAAGCTCC 262
 Oy 21 ArgArgLeuGluIleThrPheValPheLeuArgAsnPheSerLeuLeuMetLeuLeuArgTyr 40

Db 263 AGAACGCTGGACATACATCTTGCTCTTGAGAATTTCCTGATGTTAGATAC 322
 QY 41 IleGlyYlsIysAsgAsgAlaThrArgPheTrpPhePrArgGlyIleThrPro 58
 Db 323 ATTGCGAAGAAAGAGGAGCACAGCATGGATTCCTGGAGGGAGACCCA 376

RESULT_4
 ABA3588
 ID ABA3588 standard; DNA; 477 BP.
 XX AC ABA3588;
 XX DT 01-FEB-2002 (first entry)
 XX DB Human breast cell single exon nucleic acid probe #2283.
 XX KW Human: microarray; single exon probe; gene expression; breast; disease;
 KW cancer; ss.
 XX OS Homo sapiens.
 XX PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JUN-2001; 2001WO-US000662.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-496933/54.

CC New spatially-addressable set of single exon nucleic acid probes for measuring gene expression in sample derived from human breast, useful for determining predisposition and/or comprises number of single exon nucleic acid probes.

XX BS Claim 1; SEQ ID NO 2283; 327pp + Sequence Listing; English.

CC The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or assessing the toxicity of chemical agents on cells. The microarray of progressing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 477 BP; 147 A; 104 C; 88 G; 138 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5.67e-34 Length: 477
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0

	DB:	4	Gaps:	0
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	4	Gaps:	0	
US-10-031-158-14 (1-58) x ABA43588 (1-477)				
QY	1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20			
Db	212 ATGCAGATGTTCCCCAACCCACTATTTCCTTCATGTGAAACAAAGCTC 271			
QY	21 ArgArgLeuGluHisthrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40			
Db	272 AGAGGCTGGCACACTTGCTCTTGGAATTTCCCTGatGTTAAGATAC 331			
QY	41 IleGlyLysLysBargArgAlaThrArgPheTrpAspProArgGlyThrPro 58			
Db	332 ATGGCAGAAGAAGAGCAACACGATTCGGATCCAGGAGGGACACCA 385			
RESULT 5				
AAK27758				
ID AAK27758 standard; DNA; 477 BP.				
XX				
AC AAK27758;				
XX				
DT 06-NOV-2001 (first entry)				
DE Human bone marrow expressed single exon probe SEQ ID NO: 2315.				
XX				
KW Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.				
KW Homo sapiens.				
OS XX				
PN WO20017276-A2.				
XX				
PD 09-AUG-2001.				
XX				
PP 30-JAN-2001; 2001WO-US000668.				
XX				
PR 04-FEB-2000; 2000US-0180312P.				
XX				
PR 26-MAY-2000; 2000US-0207458P.				
PR 30-JUN-2000; 2000US-00608408.				
PR 03-AUG-2000; 2000US-00632366.				
PR 21-SEP-2000; 2000US-0234687P.				
PR 04-OCT-2000; 2000GB-00024263.				
XX				
PA (MOLE-) MOLECULAR DYNAMICS INC.				
XX				
PI Penn SG, Hanzel DK, Chen W, Rank DR;				
XX				
DR WPI; 2001-488900/53.				
XX				
PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.				
XX				
PS Example 4; SEQ ID NO 2315; 658pp + Sequence Listing; English.				
XX				
CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. These can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukemia and myeloma. The present sequence is one of the probes of the invention				
CC Sequence 477 BP; 147 A; 104 C; 88 G; 138 T; 0 U; 0 Other;				
SQ Alignment Scores:	5.67e-34	Length:	477	
Pred. No.:	307.00	Matches:	58	
Score:	100.00%	Conservative:	0	
Percent Similarity:	100.00%	Mismatches:	0	
Best Local Similarity:	100.00%	Indels:	0	
Query Match:	100.00%			
DB: 4	Mismatches: 0	Indels: 0	Gaps: 0	
US-10-031-158-14 (1-58) x AAK27758 (1-477)				
QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20				
Db 212 ATGCAGATGTTCCCCAACCCACTATTTCCTTCATGTGAAACAAAGCTC 271				
QY 21 ArgArgLeuGluHisthrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40				
Db 272 AGAGGCTGGCACACTTGCTCTTGGAATTTCCCTGatGTTAAGATAC 331				
QY 41 IleGlyLysLysBargArgAlaThrArgPheTrpAspProArgGlyThrPro 58				
Db 332 ATGGCAGAAGAAGAGCAACACGATTCGGATCCAGGAGGGACACCA 385				
RESULT 6				
AB02210 ABS02210 standard; DNA; 477 BP.				
XX				
AC ABS02210;				
XX				
DT 19-AUG-2002 (first entry)				
XX				
DE Human genome-derived single exon probe from lung SEQ ID NO 2201.				
XX				
KW Human; ds; Single exon probe; asthma; lung cancer; COPD; IUD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome; pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia; primary ciliary dyskinesia; pulmonary hypertension; hyaline membrane disease.				
XX				
OS Homo sapiens.				
XX				
PN WO200186003-A2.				
XX				
PR 04-FEB-2000; 2000US-0180312P.				
XX				
PR 26-MAY-2000; 2000US-0207458P.				
PR 30-JUN-2000; 2000US-00608408.				
PR 03-AUG-2000; 2000US-00632366.				
PR 21-SEP-2000; 2000US-0234687P.				
PR 04-OCT-2000; 2000GB-00024263.				
XX				
PA (MOLE-) MOLECULAR DYNAMICS INC.				
XX				
PI Penn SG, Hanzel DK, Chen W, Rank DR;				
XX				
DR WPI; 2002-114183/15.				
XX				
PT Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.				
XX				
PS Claim 1; SEQ ID NO 2201; 634pp; English.				
XX				
CC The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements, or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes ; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung				

CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridization of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberculous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karakener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 XX at ftp://wipo.int/pub/published_pct_sequences

Sequence 477 BP; 147 A; 104 C; 88 G; 138 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5 67e-34 Length: 477
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 DB: 6 Indels: 0
 Gaps: 0

US-10-031-158-14 (1-58) x ABS02210 (1-477)

QY 1 MetGluMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
 DB 212 ATGCAGATGTTTCCCCAACGCCACTATTTCCTCAATTGCGAAACAAGCTCC 271

QY 21 ArgArgLeuGluHisThrPheValPheLeuGlnPheSerLeuMetLeuLeuArgTyr 40
 DB 272 AGAGGGTGGACATACCTTGCTCTTGAGAAATTTCCTGTGAGTTTAAGATAC 331

QY 41 IleGlyLysSbArgGalaIthrArgPheProArgGlyThrPro 58
 DB 332 ATTGGCAGAAGAAGAGCACACGGATCTGGATCCAGGGGGACACCA 385

RESULT 7

ABV28618/C
 ID ABV28618 standard; cDNA; 539 BP.

AC ABV28618;
 DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 28609.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 PD 23-AUG-2001.
 PP WO200160860-A2.

20-FEB-2001; 2001WO-US005171.

XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUN-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX PA (MILU-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PT schlegel R, Endge WO, Monahan JE;
 XX DR
 XX WPI; 2001-662795/76.
 XX
 The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV6213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC determining whether prostate cancer has metastasized in a patient;
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 Sequence 539 BP; 134 A; 104 C; 106 G; 195 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 6 6.8e-34 Length: 539
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 DB: 5 Indels: 0
 Gaps: 0

US-10-031-158-14 (1-58) x ABV28618 (1-539)

QY 1 MetGluMetPheProProSerProLeuPhePheLeuGlnLeuLeuLeuGlnSerSer 20
 DB 410 ATGCAGATGTTTCCCCAACGCCACTATTTCCTCAATTGCGAAACAAGCTCC 351

QY 21 ArgArgLeuGluHisThrPheValPheLeuGlnPheSerLeuMetLeuLeuArgTyr 40
 DB 350 AGRAGGGTGGACATACCTTGCTCTTGAGAAATTTCCTGTGAGTTTAAGATAC 291

QY 41 IleGlyLysSbArgGalaIthrArgPheProArgGlyThrPro 58
 DB 290 ATTGGCAGAAGAAGAGCACACGGATCTGGATCCAGGGGGACACCA 237

RESULT 8

ABV2291/c
 ID ABV2291 standard; cDNA; 539 BP.

XX
 AC ABV2291;
 XX
 DT 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 22782.

DB
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 PD WO200160860-A2.

PP WO200160860-A2.

XX
 XX
 PD
 23-AUG-2001.
 XX
 XX
 PR
 20-FEB-2001; 2001WO-US005171.
 XX
 XX
 PR
 17-FEB-2000; 2000US-0183319P.
 PR
 16-MAR-2000; 2000US-018982P.
 PR
 25-MAY-2000; 2000US-0207434P.
 PR
 09-JUN-2000; 2000US-0211314P.
 PR
 18-JUL-2000; 2000US-021007P.
 PR
 13-DEC-2000; 2000US-0255281P.
 XX
 PA
 (MILL-) MILLENIUM PREDICTIVE MEDICINE INC.
 XX
 PT
 schlegel R., Endge WO, Monahan JE;
 XX
 DR
 WPI; 2001-662795/76.
 XX
 PT
 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS
 Claim 1; Page 4022; 11750PP; English.
 XX
 CC
 The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV2213) of the specification or its complement. (1) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the efficacy of progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 CC
 Sequence 539 BP; 134 A; 104 C; 106 G; 195 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 6.68e-34 Length: 539
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB:
 5
 US-10-031-158-14 (1-58) x ABV22791 (1-539)
 QY
 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db
 410 ATGGAGATGTTCCCAAGCCACTATTTCTCTCAATTGTGTCACAAAGCTCC 351
 QY
 21 ArgArgLeuGluHisthRheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyr 40
 Db
 350 AGAAGGCTGGRACATACCTTGCTCTTGAGAATTTCCCTGATGTATTAGATAC 291
 QY
 41 IleGlyLysLysArgArgAlaThrArgPheTrpAspProArgGlyGlyThrPro 58
 Db
 290 ATTGGCAAGAAAGAGAGCAAGCAGATGTTGGATCCAGGGGAAACCA 237
 RESULT 9
 AAQ66888
 ID AAQ66888 standard; cDNA; 825 BP.
 AC AAQ66888;
 XX
 DT
 25-MAR-2003 (revised)
 DT
 02-FEB-1995 (first entry)
 XX
 DB
 Human Lymphocyte clone G 115 soluble TCR gamma chain.
 XX
 KW
 Soluble T cell receptor; TCR; pathological T lymphocyte; PCR primer;

KW
 polymerase chain reaction; leukaemia; Burkitt's lymphoma;
 KW
 autoimmune disease; cell typing; gamma; delta; lymphocyte G115;
 KW
 Mycobacterium tuberculosis; ss.
 XX
 OS
 Homo sapiens.
 XX
 FR
 Key Location/Qualifiers
 FT 1..825 /*tag= a
 CDS /product= "soluble_Vgamma_chain"
 XX
 DN W09412648-A2.
 XX
 DR 09-JUN-1994.
 XX
 PR 25-NOV-1993; 93WO-FR001165.
 XX
 PR 25-NOV-1992; 92FR-00014203.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (IMMU-) IMMUNOTEC SA.
 XX
 PI Bonneville M;
 XX
 DR WPI; 1994-200276/24.
 DR P-PSDB; AAR55705.
 XX
 PR prodn. of soluble T receptors lacking the trans-membrane region - by co-transfection of host cells with truncated sub unit DNA, for diagnosis and treatment of pathological T cell proliferation.
 XX
 PS Example 1; Fig 2B; 41PP; French.
 CC The human lymphocyte clone gamma-delta-s Gil5 expresses T cell receptors v9JPcGamma/v2D9JICdelta. The soluble delta and gamma chains have the sequences AAQ66887 and AAQ66888, respectively. This clone, which kills Burkitt's lymphoma ("Daudi") cells and recognises an antigen present in water-soluble extracts of *M. tuberculosis*, was used for the construction of gamma-delta-s genes and expression of soluble T cell receptors. The soluble TCRs (i.e. lacking the transmembrane region) are useful in diagnosis (esp. cell typing) and treatment of conditions involving T cell proliferation, e.g. leukaemia, lymphoma or some autoimmune diseases.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC Sequence 825 BP; 267 A; 178 C; 176 G; 204 T; 0 U; 0 Other;
 XX
 SQ Sequence 825 BP; 267 A; 178 C; 176 G; 204 T; 0 U; 0 Other;
 DB:
 5
 US-10-031-158-14 (1-58) x AAQ66888 (1-825)
 QY
 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db
 440 ATGCAGATGTTCCCAAGCCACTATTTCTCTCAATTGTGTCACAAAGCTCC 499
 QY
 21 ArgArgLeuGluHisthRheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyr 40
 Db
 500 AGAAGGCTGGRACATACCTTGCTCTTGAGAATTTCCCTGATGTATTAGATAC 559
 QY
 41 IleGlyLysLysArgArgAlaThrArgPheTrpAspProArgGlyGlyThrPro 58
 Db
 560 ATTGGCAAGAAAGAGAGCAACGAGATCTGGATCCAGGGGAAACCA 613
 RESULT 10
 ACF35988
 ID ACF35988 standard; cDNA; 825 BP.
 XX
 AC ACF35988;

XX DT 20-NOV-2003 (first entry)

XX DB Human T cell receptor Vgamma9 cDNA sequence.

XX KW T cell receptor; TCR; gastrointestinal; antiinflammatory; cytostatic; tuberculostatic; dermatological; antibacterial; virucide; gynaecological; cell therapy; Vgamma; human; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1. 825 /tag= a /product= "TCR Vgamma9"

XX PN WO2003060097-A2.

PD 24-JUL-2003.

PP 10-JAN-2003; 2003WO-US000728.

PR 10-JAN-2002; 2002US-0347285P.

XX PA (NAJU-) NAT JEWISH MEDICAL & RES CENT.

XX PI O'brien RU, Born MK, Roark CL, Aydintug MK;

DR WPI; 2003-598525/56.

DR P-PSDB; ABR82194.

XX PT Regulating a gammadelta T-cell mediated immune response in a mammal, useful for treating inflammation in intestine, skin, lungs or reproductive tract, comprises administering to the mammal a soluble gammadelta T cell receptor.

XX PT Example; Page 64-65; 71pp; English.

CC The invention relates to regulating a gammadelta T-cell mediated immune response in a mammal and involves administering to the mammal a soluble gammadelta T cell receptor (TCR). The method is useful for treating patients having, or are at risk of developing an intestinal condition, e.g. Crohn's disease, ischaemic colitis, irritable bowel disease, and colon cancer; a lung condition associated with inflammation such as airway hyperresponsiveness, pneumonia, tuberculosis, and a primary or metastatic lung tumour; a skin condition associated with inflammation such as skin lesion caused by bacterial infection, viral infection or laceration, and a skin cancer; or a condition associated with inflammation of the reproductive tract such as infection caused by bacterial or viral infection that involve the epithelial mucosal lining, tubal infection, preventing tubal factor infertility, and a cancer selected from ovarian, cervical, uterine, prostate or testicular cancers. Sequences ACMP5987-988 represent human TCR Vgamma chain cDNAs used in the present invention.

XX SO Sequence 825 BP; 267 A; 178 C; 176 G; 204 T; 0 U; 0 Other;

Alignment Scores:

Pred. No. :	1.19e-33	Length:	825
Score:	307.00	Matches:	58
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9	Indels:	0
Gaps:	0		

DB: US-10-031-158-14 (1-58) x ACMP5988 (1-825)

QY 1 MetGlnMetPheProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20

DB 440 ATGCAGATGTTCCCCAACCCACATTCTCTCTCTGAAACAAAGCTCC 499

QY 21 ArgArgLeuGluIleThrPheValPheLeuArgSerPhenSerLeuMetIleLeuIleGlyTyr 40

DB 134 AGAAGGCTGGACATACCTTGTCCTCGAAATTTCCTCATGTTATTAGATAC 193

QY 41 IleGlyLysysArgGalaThrArgPheTrpPheTrpPheTrpPheTrpPheTrpArgGlyIlePro 58

DB 194 ATGCCAGAAAGAGAGAGACACGATCTGGATCCCAAGGAGGAGCACCA 247

RESULT 12

ADB75580 standard; cDNA; 1027 BP.

XX ADB75580;

XX DT 04-DBC-2003 (first entry)

XX DB Prostate cancer marker cDNA.

XX KW Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX OS Homo sapiens.

XX XX WO2003009814-A2.

XX PD 06-FEB-2003.

XX XX PR 25-JUL-2002; 2002WO-US023913.

XX PR 25-JUL-2001; 2001US-0307982P.

XX PR 22-AUG-2001; 2001US-0314356P.

XX PR 25-SEP-2001; 2001US-0325020P.

XX PR 12-DEC-2001; 2001US-0341746P.

XX PR 05-MAR-2002; 2002US-0362158P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Schlegel R, Monahan JE, Endgeorge WO, Gannavarapu M, Gorbatchava B;

XX PI Hoersh S, Kamatkar S, Wonsley AM, Glatt K, Zhao X, Anderson D;

XX DR XX WPI; 2003-248033/24.

XX PT New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX PS Disclosure; SEQ ID NO 404; 99pp; English.

XX XX CC The invention relates to newly discovered cancer markers associated with

CC the cancerous state of prostate cells. Also disclosed is a method of

CC assessing whether a patient is afflicted with prostate cancer. The method

CC of the invention involves assessing whether a patient is afflicted with

CC prostate cancer by comparing the level of expression of a marker in a

CC patient sample and the normal level of expression of the marker in a

CC control non-prostate cancer sample, where a significant increase in the

CC level of expression of the marker in the patient sample and the normal

CC level indicates that the patient is afflicted with prostate cancer.

CC Nucleic acids of the invention are useful for diagnosing or treating

CC prostate cancer, and may be useful in gene therapy. Sequences given in

CC ADB75177-AB75631 represent marker cDNA and protein. Note: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1027 BP; 307 A; 232 C; 200 G; 288 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.59e-33 Length: 1027
Score: 307.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-031-158-14 (1-58) x ADB75580 (1-1027)

Qy 1 MetGlnMetPheProProSerProLeuIlePhePhePheLeuGluGluLeuIleGlnSerSer 20
Db 74 ATGGCAGATGTTGCCCAAGCCACTATTTCCTCTTCAATGCTGAACTAAGCTC 133Qy 21 ArgArgLeuGluLysIlePheValPheLeuArgSerSerLeuMetIleLeuLeuArgTyr 40
Db 134 AGAGGCTCGAACATACCTTGCTTCTTGAGAAATTTCCTGATGTTATTAGATA 193

QY

41 IleGlyXysIySArgArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58
ID 194 ATTGGCAAGAAAGAGACACAGCATCTGGATCCAGGAGGGAAACACCA 247

Db ABV26485/C

16-SEP-2002 Human prostate expression marker cDNA 26476.

XX XX XX

XX ABV26485; Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX XX XX

XX Homo sapiens.

XX XX XX

XX WO200160860-A2.

XX 23-AUG-2001.

XX XX XX

XX Homo sapiens.

XX XX XX

XX 20-FEB-2001; 2001WO-US005171.

XX XX XX

XX 17-FEB-2000; 2000US-0183319P.

XX XX XX

XX 16-MAR-2000; 2000US-0189862P.

XX XX XX

XX 25-MAY-2000; 2000US-0207454P.

XX XX XX

XX 09-JUN-2000; 2000US-0211314P.

XX XX XX

XX 18-JUL-2000; 2000US-0219007P.

XX XX XX

XX 13-DEC-2000; 2000US-0255281P.

XX XX XX

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endgeorge WO, Monahan JE;

XX XX DR WPI; 2001-662795/76.

XX XX PS Claim 1; Page 5351; 11750pp; English.

XX XX XX

The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the progression

CC of prostate cancer in a patient; (c) assessing the efficacy

CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC determining whether prostate cancer has metastasized in a patient;

CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 1316 BP; 369 A; 282 C; 300 G; 365 T; 0 U; 0 Other;

XX XX Alignment Scores:
Pred. No.: 2.22e-33 Length: 1316Score: 307.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-031-158-14 (1-58) x ABV26485 (1-1316)

Qy 1 MetGlnMetPheProProSerProLeuIlePhePhePheLeuGluGluLeuIleGlnSerSer 20
Db 562 ATGCAGATGTTGCCCAAGCCACTATTTCCTCTTCAATGCTGAACTAAGCTC 503

QY 21 ArgArgLeuGluHisthrPheValpheLeuLysPheSerLeuMetLeuLeuLysGlnSer 40
 Db 502 AGAGGCTGGACATCCTTCCTTGAAATTTCCTGATGTTAGATAC 443

QY 41 IleGlyLysLysArgArgAlaThrArgPheTrpProArgArgLysThrPro 58
 Db 442 ATGGCAAGAAGAGCACACCGATTCTGGATCCAGGAGGAACCCA 389

RESULT 14
 ID ABV25093/c standard; cDNA; 1316 BP.
 XX
 AC ABV25093;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25084.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX
 OS Homo sapiens.
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PP 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-025281P.

XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-66275/76.

XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 4881; 1175pp; English.

XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABv00010-ABv62213) of the
 CC specification or its complement. (1) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 1316 BP; 369 A; 282 C; 300 G; 365 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.22e-33 Length: 1316
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5 Indels: 0
 Gaps: 0

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLysGlnSer 20
 Db 562 ATGCAGATGTTCCCAAGCCACTATTTCTCTCAATGCTGAAACAGCTC 503

QY 21 ArgArgLeuGluHisthrPheValpheLeuLysPheSerLeuMetLeuLeuLysGlnSer 40
 Db 502 AGAGGCTGGACATCCTTCCTTGAAATTTCCTGATGTTAGATAC 443

QY 41 IleGlyLysLysArgArgAlaThrArgPheTrpProArgArgLysThrPro 58
 Db 442 ATGGCAAGAAGAGCACACCGATTCTGGATCCAGGAGGAACCCA 389

RESULT 15
 ID ADL06443 standard; cDNA; 1395 BP.
 XX
 AC ADL06443;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #23.
 XX
 KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
 KW cancer; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016225-A2.
 XX
 PD 26-FEB-2004.
 XX
 PR 19-AUG-2003; 2003WO-US025892.
 XX
 BR 19-AUG-2002; 2002US-0404809P.
 BR 21-AUG-2002; 2002US-0405645P.
 PR 23-SEP-2002; 2002US-0413192P.
 PR 15-OCT-2002; 2002US-0413008P.
 PR 15-NOV-2002; 2002US-0416847P.
 PR 02-JUL-2003; 2003US-0484959P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PT Desauvage RJ, Frantz G, Hillian KJ, Polakis P, Polson A, Smith V;
 PT Spencer SD, Wu TD, Zhang Z;
 XX
 DR WPI; 2004-257144/24.
 DR P-PSDB; ADL06223.

XX
 PT New antibody that binds to a tumor-associated antigenic target (TAT)
 PT polypeptide, useful for preparing a composition for diagnosing or
 PT treating cancer.
 XX
 PS Claim 1; SEQ ID NO 23; 319P; English.

XX
 CC The present invention relates to the isolation of human tumour-associated
 CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
 CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
 CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
 CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
 CC produced in bacteria or in CHO cells and induces death of a cell to which
 CC it binds. The antibody is useful for preparing a composition for
 CC diagnosing or treating tumours and cancer. The present sequence
 CC represents a human TAT cDNA sequence of the invention.

XX
 SQ Sequence 1395 BP; 405 A; 324 C; 286 G; 380 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.41e-33 Length: 1395
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

US-10-031-158-14 (1-58) x ABV25093 (1-1316)

DB: 10 Gaps: 0

US-10-031-158-14 (1-58) x ADB08798 (1-2658)

Qy 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLeuGlnSerSer 20
 Db 2381 ATGCAGATGTTCCCCAACGCCACATTCTTCATCTTGAACTTGTAAAGATAC 2322

Qy 21 ArgArgLeuGluHisThrPheValPheLeuArgAspPheSerLeuMetLeuLeuArgTyr 40
 Db 2321 AGAAGGCTGGAACTACCTTGTCTTGAAATTCTCGATGTTAAAGATAC 2262

Qy 41 IleGlyLysSarGargAlaThrArgPheTrpAspProArgGlyThrPro 58
 Db 2261 ATTGGCAAGAAAGAGCACACGAATCTGGATCCAGGGAAACCCA 2208

RESULT 18
 ABV2013/c
 ID ABV25013 standard; CDNA; 486 BP.

AC ABV2013;
 XX
 AC ABV2013;

XX DT 16-SEP-2002 (first entry)

DB Human prostate expression marker CDNA 25004.
 XX
 KW Human; prostate cancer; cytosatic; carcinogen; pharmacodynamic marker;
 XX pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX
 PN WO200160860-A2.

PD 23-AUG-2001:
 XX
 PR 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.

XX (MILLI-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;
 XX DR
 PR 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.

PS Claim 1; Page 4846; 11750PP; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
 CC specification or its complement. (1) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX Sequence 486 BP; 117 A; 94 C; 101 G; 174 T; 0 U; 0 Other;

SQ Alignment Scores:

Pred. No.: 1.55e-33 length: 486

Score: 304.00 Matches: 57
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 98.28% Misnatches: 0
 Query Match: 99.02% Indels: 0
 DB: 5 Gaps: 0

US-10-031-158-14 (1-58) x ABV25013 (1-486)

Qy 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLeuGlnSerSer 20
 Db 411 ATGCAGATGTTCCCCAACGCCACATTCTTCATCTTGAAATTCTCGATGTTAAAGATAC 352

Qy 21 ArgArgLeuGluHisThrPheValPheLeuArgAspPheSerLeuMetLeuLeuArgTyr 40
 Db 351 AGAAGGCTGGAACTACCTTGTCTTGAAATTCTCGATGTTAAAGATAC 292

Qy 41 IleGlyLysSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 291 ATTGGCAAGAAAGAGCACACGAATCTGGATCCAGGGAAACCCA 238

RESULT 19
 ABV47985
 ID ABV47985 standard; DNA; 316 BP.

AC ABV47985;
 XX
 PR 01-FEB-2002 (first entry)

DE Human breast cell single exon nucleic acid probe #6680.
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 XX cancer; ss.
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0234359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 BA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR
 WPI; 2001-496333/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.

XX
 PS Claim 4; SEQ ID NO 6680: 327PP + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC progressing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag

CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a single exon
 CC nucleic acid probe of the invention. Note: The sequence data for this
 CC patient did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 316 BP; 112 A; 65 C; 62 G; 77 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.67e-33

Length: 316

Score: 302.00

Matches: 57

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Best Local Similarity: 100.00%

Indels: 0

Query Match: 98.37%

Gaps: 4

DB: US-10-031-158-14 (1-58) x ABA47985 (1-316)

QY 2 GluMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSerArg 21

Db 2 CAGATGTTCCCCAACCCACTATTTCCTCAATTGTGAAACAAAGCTCCAGA 61

QY 22 ArgLeuGluIleThrPheValPheLeuArgAsnPhsSerLeuMetLeuLeuArgTyrIle 41

Db 62 AGGCTGGACATACCTTGCTCTGAGAATTTTCCCTGATGTTAGATCATT 121

QY 42 GlyLysIysSArgArgAlaThrArgPheTrpAspProArgArgGlyLysThrPro 58

Db 122 GCGAAGAAAGAGAGAGCACACGATCTGGATGCCAGGAAGGAAACACCA 172

RESULT 20

AAK40015 ID AAK40015 standard; DNA; 316 BP.

AC AAK40015; XX DT 06-NOV-2001 (first entry)

XX DE Human bone marrow expressed single exon probe SEQ ID NO: 14572.

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;

microarray; cancer; leukaemia; lymphoma; myeloma; ss.

OS Homo sapiens.

PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.

XX PR 04-FEB-2000; 2000US-0180312P.

PR 24-MAY-2000; 2000US-020745GP.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00633156.

PR 27-SEP-2000; 2000US-0234687P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 14572; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention

XX SQ Sequence 316 BP; 112 A; 65 C; 62 G; 77 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.67e-33

Length: 316

Score: 302.00

Matches: 57

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Best Local Similarity: 100.00%

Indels: 0

Query Match: 98.37%

Gaps: 4

DB: US-10-031-158-14 (1-58) x AAK40015 (1-316)

QY 2 GluMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSerArg 21

Db 2 CAGATGTTCCCCAACCCACTATTTCCTCAATTGTGAAACAAAGCTCCAGA 61

QY 22 ArgLeuGluIleThrPheValPheLeuArgAsnPhsSerLeuMetLeuLeuArgTyrIle 41

Db 62 AGCTGAAACATACCTTGCTCTGAGAATTTTCCCTGATGTTAGATCATT 121

QY 42 GlyLysIysSArgArgAlaThrArgPheTrpAspProArgArgGlyLysThrPro 58

Db 122 GCGAAGAAAGAGAGAGCACACGATCTGGATGCCAGGAAGGGAAACACCA 172

RESULT 21

AAK4101 ID ABS14101 standard; DNA; 316 BP.

AC ABS14101; XX DT 19-AUG-2002 (first entry)

XX DB Human genome-derived single exon probe ORF from lung SEQ ID No 14092.

XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; IBD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomomatis; Kartagener syndrome;

KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease; open reading frame; ORF;

XX OS Homo sapiens.

XX PN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-020745GP.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234677P.

PR 27-SEP-2000; 2000US-0236339P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2002-114183/15.

XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 CC measure gene expression in human lung samples.

XX
 PS Claim 4; SEQ ID NO 14092; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 12614 nucleic acid sequences mentioned in the specification, or their
 complements or the 12387 open reading frames derived from the 1.614
 probes. Also included are a microarray comprising the novel set of probes
 ; the novel set of probes which hybridise at high stringency, to a nucleic
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung; comprising (a) contacting the array with a
 collection of detectably labeled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array, identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridisation of detectably
 labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying exons from genomic sequence by the method
 above and (b) measuring the expression of each of the exons in several
 tissues and/or cell types using hybridization to a single exon
 microarray having a probe with the exon, where a common pattern of
 expression of the exons in the tissues and/or cell types indicates that
 the exons should be assigned to a single gene; a peptide comprising one
 of 12011 sequences, mentioned in the specification, or encoded by the
 probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 lung derived mRNA and for the study of lung diseases such as asthma, lung
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 Pudlak syndrome, sarcoidosis, pulmonary hamosiderosis, pulmonary
 histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,
 Kartagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary
 dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 present sequence is a single exon probe open reading frame of the
 invention. Note: The sequence data for this patent did not form part of
 the printed specification, but was obtained in electronic format directly
 from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequences

XX Sequence 316 BP; 112 A; 65 C; 62 G; 77 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.67e-33 Length: 316
 Score: 302.00 Matches: 57
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 98.37% Mismatches: 0
 Query Match: 6 Indels: 0
 DB: 6 Gaps: 0

US-10-031-158-14 (1-58) x ABS14101 (1-316)

Qy 2 GluMetPheProProSerProLeuPhePheLeuGlnLeuLeuLeuGlnSerSer 21
 Db 2 CAGATGTTCCGCCAACGCCACTATTTCTTCATGCTGAACAAAGCTCCAGA 61

Qy 22 ArgLeuGluHisThrPheValPheLeuArgIleAsnPhosSerLeuMetLeuLeuArgTyrile 41
 Db 62 AGGCTGGAACTTACCTTGTTCTCTGAGAAATTCTCCGATGTATTAAGTCATT 121

Qy 42 GlyLysSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 122 GCGAAGAGAGAGAGCACAGATTCTGGATCCAGGGAGAACACCA 172

RESULT 22
 ABV43475/C
 ID ABV43475 standard; cDNA; 569 BP.
 XX
 AC ABV43475;
 XX
 DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 43466.
 DE Human prostate expression marker cDNA 43466.
 XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS WO200160860-A2.
 PN 23-AUG-2001.
 PD 20-FEB-2001; 2001WO-US005171.
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0183862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0215007P.
 PR 13-DEC-2000; 2000US-0255281P.
 PR (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endge WO, Monahan JB;
 DR WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 CC prostate cells and correlating with presence of prostate cancer, stage of prostate cancer.
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX BS Claim 1; Page 862; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 specification or its complement. (I) is useful for: (a) assessing whether
 a patient is afflicted with prostate cancer; (b) monitoring the
 progression of prostate cancer in a patient; (c) assessing the efficacy
 of a test compound to inhibit prostate cancer in a patient; (d) assessing
 the efficacy of a therapy for inhibiting prostate cancer in a patient;
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound;
 (g) determining whether prostate cancer has metastasized in a patient; (h)
 assessing the aggressiveness or indolence of prostate cancer in a patient;
 (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX Sequence 569 BP; 141 A; 109 C; 120 G; 199 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.37e-32 Length: 569
 Score: 298.00 Matches: 57
 Percent Similarity: 98.28% Conservative: 0
 Best Local Similarity: 98.28% Mismatches: 1
 Query Match: 97.07% Indels: 0
 DB: 5 Gaps: 0

US-10-031-158-14 (1-58) x ABV43475 (1-569)

Qy 1 MetGluMetPheProProSerProLeuPhePheLeuGlnLeuLeuLeuGlnSerSer 20
 Db 460 ATGCAGATGTTCTCCCAAGCCACTATTTCTCTTCATGCTGAACAAAGCTCC 401

Qy 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPhosSerLeuMetLeuLeuArgTyr 40
 Db 400 AGAAGCTGGACATACTTGTCCTGAGAAATTCTCCGATGTTAAGTC 341

Qy 41 LleGlyLysSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 340 ATTGGCAAGAAAGAGACAGATTCCTGGATCCAGGGAGAACACCA 287

RESULT 23
 ABL6007
 ID ABL6007 standard; DNA; 1421 BP.

AC ABL65007; AC

XX 15-MAY-2002 (first entry) PS

XX DR Lung cancer related gene sequence SEQ ID NO:3344. CC

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; CC neoplastic agent. The method involves exposing cells to a chemical agent CC to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164 CC to ABU0110), or I is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytotoxic CC cytotoxic; gene therapy; antineoplastic; Wil'm's tumour; adenocarcinoma; CC gene; ds.

XX KW Homo sapiens. CC

XX WO200194629-A2. CC

XX PN 13-DEC-2001. CC

XX PD 30-MAY-2001; 2001WO-US010838. CC

XX XX SQ 05-JUN-2000; 2000US-0209473P. CC

PR 05-JUN-2000; 2000US-0209531P. CC

PR 18-SEP-2000; 2000US-0233133P. CC

PR 18-SEP-2000; 2000US-02333617P. CC

PR 20-SEP-2000; 2000US-0234009P. CC

PR 20-SEP-2000; 2000US-0234034P. CC

PR 22-SEP-2000; 2000US-0234052P. CC

PR 22-SEP-2000; 2000US-0234509P. CC

PR 22-SEP-2000; 2000US-0234567P. CC

PR 25-SEP-2000; 2000US-0234923P. CC

PR 25-SEP-2000; 2000US-0234924P. CC

PR 25-SEP-2000; 2000US-0235077P. CC

PR 25-SEP-2000; 2000US-0235082P. CC

PR 25-SEP-2000; 2000US-0235134P. CC

PR 25-SEP-2000; 2000US-0235280P. CC

PR 26-SEP-2000; 2000US-0235637P. CC

PR 26-SEP-2000; 2000US-0235638P. CC

PR 27-SEP-2000; 2000US-0235720P. CC

PR 27-SEP-2000; 2000US-0235840P. CC

PR 27-SEP-2000; 2000US-0235863P. CC

PR 28-SEP-2000; 2000US-0236028P. CC

PR 28-SEP-2000; 2000US-0236032P. CC

PR 28-SEP-2000; 2000US-0236034P. CC

PR 28-SEP-2000; 2000US-0236109P. CC

PR 21-SEP-2000; 2000US-0236611P. CC

PR 29-SEP-2000; 2000US-0236842P. CC

PR 29-SEP-2000; 2000US-0236891P. CC

PR 02-OCT-2000; 2000US-0237172P. CC

PR 02-OCT-2000; 2000US-0237173P. CC

PR 02-OCT-2000; 2000US-0237278P. CC

PR 02-OCT-2000; 2000US-0237294P. CC

PR 02-OCT-2000; 2000US-0237316P. CC

PR 03-OCT-2000; 2000US-0237425P. CC

PR 03-OCT-2000; 2000US-0237598P. CC

PR 03-OCT-2000; 2000US-0237604P. CC

PR 03-OCT-2000; 2000US-0237606P. CC

PR 01-NOV-2000; 2000US-0244867P. CC

PR 01-NOV-2000; 2000US-0245084P. CC

XX PA (AVHL-) AVALON PHARM. XX

XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S; XX Soppet DR, Waever Z; XX

XX DR WPI; 2002-188264/24. XX

XX PT Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a Signature Gene Set. XX

XX PR 01-Nov-2000; 2000US-0245084P. XX

XX PR 03-JUL-2003. XX

XX PR 10-DEC-2002; 2002WO-US039555. XX

XX PR 10-DEC-2001; 2001US-0339739P. XX

PR 11-DEC-2001; 2001US-0339453P. XX

PR 14-MAR-2002; 2002US-0365091P. XX

PR 14-MAR-2002; 2002US-0365384P. XX

PR 12-APR-2002; 2002US-0372381P. XX

PR 22-APR-2002; 2002US-00128558. XX

XX Claim 1; SEQ ID NO 3344; 44pp; English. XX

XX The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 to ABU0110), or I is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytotoxic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wil'm's tumour. XX

XX Sequence 1421 BP; 419 A; 325 C; 292 G; 385 T; 0 U; 0 Other; XX

XX Alignment Scores: XX

Pred. No.:	1-74e-31	Length:	1421
Score:	2.94.00	Matches:	55
Percent Similarity:	98.28%	Conservative:	2
Best Local Similarity:	94.83%	Mismatches:	1
Query Match:	95.77%	Indels:	0
DB:	6	Gaps:	0

XX US-10-031-158-14 (1-58) x ABL65007 (1-1421) XX

QY 1 MercinMatPheProProSerProLeuPhePhePheLeuGlnIleuLeuIysGlnSerSer 20

Db 423 ATGCAGATGTTTCCCCAACGCCCACTATTTCCTCTCTCATGGTGAACAAACTCC 482

QY 21 ArgArgLysLysThrValPheLeuArgArgSerLeuMetLeuArgArgTrp 40

Db 483 AGAAGGCTGAGACATACCTTGCTCTTGAGAATTTCCAGATAATTAGATAC 542

QY 41 IleGlyLysLysArgGargLysArgPheTrpAspProArgGlyThreon 58

Db 543 TTGGCAAGAAAGAGAGCAGCGATCTGGATCCAGGAGGGAGCACCA 596

XX RESULT 24 XX

XX ADE06987 ID ADE06987 standard; DNA; 1560 BP. XX

XX ADE06987; AC

XX DT 29-JAN-2004 (first entry) XX

XX Novel coding sequence (useful for identifying genetic disorders) #53. XX

XX novel gene; novel protein; tissue marker; molecular weight marker; XX novel gene; novel protein; tissue marker; genetic disorder; gene; db. XX chromosome marker; genetic disorder; gene; db. OS Unidentified. OS

XX PN WO200305152-A2. PN

PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QH, Wang J;
 PI Ghosh M, Xue AJ, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI; 2003-569235/53.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
 PT
 PS Claim 1; SEQ ID NO 53; 117pp; English.

The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the invention.

CC Sequence 1560 BP; 444 A; 363 C; 322 G; 431 T; 0 U; 0 Other;

XX

Alignment Scores:
 Pred. No.: 1.97e-31 Length: 1560
 Score: 294.00 Matches: 55
 Percent Similarity: 98.28% Conservative: 2
 Best Local Similarity: 98.83% Mismatches: 1
 Query Match: 95.77% Indels: 0
 DB: 10 Gaps: 0

US-10-031-158-14 (1-58) x ADB06987 (1-1560)

Qy 1 MetGlnMetPheProProSerProleuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db 559 ATGCAGATGTTCCTCCAAGGCCACTATTTCCTCTCTCATGGAAACAAACTCC 618

Qy 21 ArgArgLeuGluLysIleThrPheValPheLeuGlnPheSerLeuMetIleLeuArgTyr 40
 Db 619 AGAACGCTGAACTACCTTGCTCTTGAGAAATTTCCTCCAGATATTAGATAC 678

Qy 41 IleGlyLysLysSargArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 679 ATTGGCAGAGAGAGAGAGCAACGATTCCTGGATCCACAGAGGGAGAACCCA 732

RESULT 25
 ABZ3581
 ID ABZ35381 standard; cDNA; 1799 BP.

AC ABZ35381;
 XX
 DT 05-FEB-2003 (first entry)

Human gene expression profile polynucleotide SEQ ID NO 492.
 XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery; bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast; tumour; microarray; genome mapping; antibiotic; antiviral; antifungal; gene expression; gene; ss.
 XX Homo sapiens.
 XX
 WO200274979-A2.

XX
 PD 26-MAR-2002.

XX
 PP 20-MAR-2002; 2002WO-US008456.

PR 20-MAR-2001; 2001US-0276947P.
 XX
 PA (ORTH-) ORTHO CLINICAL DIAGNOSTICS INC.
 XX
 PI Wan J, Wang Y;
 XX
 DR WPI; 2002-740862/80.

New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.

PT Example 3; Page 634-635; 850PP; English.

CC The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, aortic endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, keratinocyte epithelium, bronchial epithelium, mammary epithelium, prostate epithelium, renal cortical epithelium, renal proximal tubule epithelium, small airway epithelium, renal epithelium, umbilical artery smooth muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, aortic smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, osteoblasts or prostate stromal cell. The gene expression profile is used for determining the level of RNA expression for a sample, determining the phenotype of a cell and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents.

CC Sequence 1799 BP; 499 A; 434 C; 396 G; 470 T; 0 U; 0 Other;

XX

Alignment Scores:
 Pred. No.: 2.39e-31 Length: 1799
 Score: 294.00 Matches: 58
 Percent Similarity: 98.31% Conservative: 0
 Best Local Similarity: 98.31% Mismatches: 0
 Query Match: 95.77% Indels: 1
 DB: 6 Gaps: 0

US-10-031-158-14 (1-58) x ABZ35381 (1-1799)

Qy 1 MetGlnMetPheProProSerProleuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db 845 ATGCAGATGTTCCTCCAAGGCCACTATTTCCTCTCATGGAAACAAAGCTCC 904

Qy 21 ArgArgLeuGluLysIleThrPheValPheLeuGlnPheSerLeuMetIleLeuArgTyr 40
 Db 905 AGAACGCTGAACTACCTTGCTCTTGAGAAATTTCCTCCAGATATTAGATAC 964

Qy 41 IleGlyLysLysSargArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 965 ATTGGCAGAGAGAGAGAGCAACGATTCCTGGATCCACAGAGGGAGAACCCA 1019

RESULT 26
 AAQ37617
 ID AAQ37617 standard; cDNA; 1080 BP.

XX
 AC AAQ37617;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-JUN-1993 (first entry)

XX
 DB TCR gamma protein (cell line MOLT-13).

XX T cell antigen receptor; TCR; IDP2; PEER; MOLT-3; immunoglobulin;
 KW cell surface; delta chain; Form 2bc; ss.
 XX Synthetic.

OS

FH Location/Qualifiers
 FT 37..1008
 FT /*tag= a
 FT /label= gamma TCR
 FT /note= "comprises S, V, N, J, CI, CII, CIII and CIV
 regions"
 XX

Key US5185250-A.
 PN 09-FEB-1993.
 PD 13-JAN-1989; 89US-0029761.
 PR 03-JUL-1986; 86US-00882100.
 PR 19-FEB-1987; 87US-00016352.
 PR 29-OCT-1987; 87US-00113256.
 PR 29-APR-1988; 88US-00187698.
 XX

PA (TCEL-) T CELL SCI INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 XX Brenner MB, Seidman J, Strominger JL, IP SH, Krangel MS, Band H;
 PT DR WPI; 1993-067162/08.
 PR-PSDB; AR32906.

PT Gamma, delta T-cell antigen receptor hetero:dimer - used to diagnose
 PT immune deficiencies e.g. AIDS and stimulate lymphocytes.
 XX Disclosure; Fig 10A-B; 99pp; English.

PS Example 11 describes the three forms of the human TCR gamma/delta. The
 new form of the human gamma/delta TCR consists of a 40 kD TCR gamma
 glycoprotein (termed Form 2bc) noncovalently associated with a TCR delta
 chain. Clone M13K corresponds to full length, in frame, gamma TCR
 transcript. (Updated 25-MAR-2003 to correct PF field.)
 XX Sequence 1080 BP; 324 A; 260 C; 231 G; 265 T; 0 U; 0 Other;
 SQ Alignment Scores:
 Pred. No.: 4.45e-31 Length: 1080
 Score: 290.00 Matches: 54
 Percent Similarity: 98.28% Conservative: 3
 Best Local Similarity: 93.10% Mismatches: 1
 Query Match: 94.46% Indels: 0
 DB: Gaps: 0

US-10-031-158-14 (1-58) x AAQ37617 (1-1080)

QY 1 MetGlnMetPheProProSerProLeuPhePhePhePheLeuGluLeuLeuGlySerSer 20
 Db 452 ATGCAGATGTTCCCAAGCCACTATTTCTCTCGATGCTGAACTAC 511

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuLeuArgTyr 40
 Db 512 AGAAGGCTGGAACTACCTTGCTGAGAAATTTCAGATTTAATAGATAC 571

QY 41 IleGlyLysBargArgAlaIleArgPheTrpAspProArgArgGlyThrPro 58
 Db 572 ATTGCAAGAAAGAGGCAACGATCTGSGATCCCGAGGGGGACCCA 625

RESULT 27 DT 29-JAN-2004 (first entry)
 ADE08798 XX Novel DNA-related contig nucleotide sequence #42.
 ID ADE08798 DE
 XX OS novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; contig; db.
 XX Unidentified.

XX WO2003054152-A2.
 PN 03-JUL-2003.
 XX PR 10-DEC-2002; 2002WO-US039555.
 XX PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-036591P.
 PR 14-MAR-2002; 2002US-036584P.
 PR 12-APR-2002; 2002US-037281P.
 PR 12-APR-2002; 2002US-037265P.
 PR 22-APR-2002; 2002US-00120558.
 PR 24-APR-2002; 2002US-0376045P.
 XX PA (HYSE-) HYSEQ INC.
 XX PT Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PT Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX DR WPI; 2003-569235/53.

XX PS New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PR in which the corresponding protein is preferentially expressed.
 XX Disclosure; SEQ ID NO 1864; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences or to map related genes to identify potential
 CC genetic disorders. The present DNA sequence was used in the
 CC exemplification of the invention.

XX Sequence 2658 BP; 745 A; 595 C; 578 G; 750 T; 0 U; 0 Other;
 SQ Alignment Scores:
 Pred. No.: 1.5e-30 Length: 2658
 Score: 290.00 Matches: 54
 Percent Similarity: 98.28% Conservative: 3
 Best Local Similarity: 93.10% Mismatches: 1
 Query Match: 94.46% Indels: 0
 DB: Gaps: 0

US-10-031-158-14 (1-58) x ADE08798 (1-2658)

QY 1 MetGlnMetPheProProSerProLeuPhePhePhePheLeuGluLeuLeuGlySerSer 20
 Db 497 ATGCAGATGTTCCCAAGCCACTATTTCTCTCGATGCTGAACTAC 556

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuLeuArgTyr 40
 Db 557 AGAAGGCTGGAACTACCTTGCTGAGAAATTTCAGATTTCCAGAATTTAATAGATAC 616

QY 41 IleGlyLysBargArgAlaIleArgPheTrpAspProArgArgGlyThrPro 58
 Db 617 ATTGCAAGAAAGAGGCAACGATCTGSGATCCCGAGGGGGACCCA 670

RESULT 28 ADP10449

ID	DB	
ADP10449 standard; DNA; 1046 BP.	133 ATGGCAGAAGAGACACCGATCTGGATCCAGGGGACACCA 186	
XX	RESULT 29	
AC	ABK64529	
XX	ID ABK64529 standard; DNA; 1586 BP.	
DT	XX	
12-AUG-2004 (First entry)	AC	
XX	ABK64529;	
KW	XX	
transplant rejection; immune system; rheumatoid arthritis; lupus;	DE	
KW	XX	
inflammatory bowel disease; multiple sclerosis; HIV; AIDS; SB.	XX	
OS	DE	
Homo sapiens.	XX	
XX	KW	
PN	XX	
XX	Human benign prostatic hyperplasia gene #424.	
PD	XX	
21-MAY-2004.	XX	
XX	XX	
PP	XX	
24-APR-2003; 2003WO-US012946.	XX	
PR	XX	
24-APR-2002; 2002US-00131831.	XX	
PR	XX	
20-DEC-2002; 2002US-0032899.	XX	
XX	XX	
(EXPR-) EXPRESSION DIAGNOSTICS INC.	XX	
PA	XX	
XX	XX	
PI	XX	
Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;	XX	
PI	XX	
Rosenberg S;	XX	
XX	XX	
DR	XX	
WPI; 2004-400724/37.	XX	
PT	XX	
Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of the genes.	XX	
PT	XX	
PT	XX	
PS	XX	
Claim 80; SEQ ID NO 458; 1762pp; English.	XX	
CC	XX	
CC	The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.	XX
SQ	XX	
Sequence 1046 BP; 314 A; 238 C; 201 G; 293 T; 0 U; 0 other;	XX	
Alignment Scores:	XX	
Pred. No.: 3.04e-30	XX	
Score: 284.00	XX	
Percent Similarity: 96.55%	XX	
Best Local Similarity: 91.38%	XX	
Query Match: 92.51%	XX	
DB: 12	XX	
Gaps: 0	XX	
US-10-031-158-14 (1-58) x ADP10449 (1-1046)	XX	
Qy 1 MetGlmMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuValGlnSer 20	XX	
Db 13 ATGCAGATGTTCGCCGAACTATTCTCTTCTGCGAACAACTCC 72	XX	
Qy 21 ArgArgLeuGluLisThrPheValPhalaugAsnPheserIleMetLeuLeuLeuGlyTyr 40	XX	
Db 73 AGAAGGTTGGAACTATCTTGCTCTGGAATTTCAGATATTGAGATA 132	XX	
Qy 41 IleGlyLysValValGlnAlaThrArgSerGlyTyrAspProArgArgGlyThrPro 58	XX	
Alignment Scores:	XX	
Pred. No.: 5.32e-30	XX	
Score: 284.00	XX	
Percent Similarity: 96.55%	XX	
Best Local Similarity: 91.38%	XX	
Query Match: 92.51%	XX	
DB: 6	XX	
Gaps: 0	XX	
US-10-031-158-14 (1-58) x ABK64529 (1-1586)	XX	

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
 DR P-PSDB; AAP91685.
 DB XX Human gamma, delta T cell antigen receptor - studied by isolation of
 553 ATCAGAGTGTTCCTCCAGCCACTTTCTCTCGATGCGAACAACTCC 612
 PT polypeptide(s), nucleic acids and monoclonal antibodies reactive with
 epitope(s).
 QY 21 ArgArgLeuGluHisThrPheValPheLeuArgPheTrpAspProArgGlyThrPro 40
 DR 613 AGAAGGCTGGACATCTTCTCTCTGAGAAATTTCAGATATTAGATAAC 672
 QY 41 IleGlyLysLysArgArgAlaThrArgPheTrpAspProArgGlyThrPro 58
 DR 673 ATGGCAAGAAAGAGAGCACACGATTCTGGATCCAGGAGGAACTCA 726
 RESULT 30 AAN91698 standard; DNA; 1080 BP.
 ID AAN91698
 XX SQ Sequence 1080 BP; 324 A; 257 C; 233 G; 266 T; 0 U; 0 Other;
 AC AAN91698;
 XX DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 26-APR-1990 (first entry)
 XX DE Sequence of MOLT-13 cells gamma T cell antigen receptor (Form 2bc).
 XX KW Human gamma T cell antigen receptor; gamma TCR; MOLT-13 cells;
 KW clone M13k.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT CDS 37..1008
 FT misc_signal 37..16
 FT misc_RNA 80..84
 FT misc_RNA 398..406
 FT misc_RNA 439..448
 FT misc_RNA 817..826
 FT misc_RNA 871..880
 FT misc_RNA 05-MAY-1989.
 XX PF 28-OCT-1988; 88WO-US003869.
 PR 29-OCT-1987; 87US-00115256.
 PR 29-APR-1988; 88US-00187698.
 XX PA (TCBL-) TCELL SCIENCES INC.
 PA (DAND) DANA-FARBER CANCER INST.
 PA (HARD) HARVARD COLLEGE.
 XX PI Brenner MB, IP SH, Seidman J;
 XX DR WPI; 1989-150856/20.

DR P-PSDB; AAP91685.
 XX Human gamma, delta T cell antigen receptor - studied by isolation of
 CC polypeptide(s), nucleic acids and monoclonal antibodies reactive with
 epitope(s).
 XX Fig 14; Page ?, 104pp; English.
 CC The CNS (tag b) codes for human gamma T cell antigen receptor polypeptide
 termed Form 2bc. The sequence can be DNA or RNA. It was prep'd. as
 follows: a cDNA library was prep'd. from MOLT-13 poly(A)+ RNA in lambda
 gt10 vector. This library was amplified on the E.coli strain C600 HfI and
 screened. cDNA clone M13k was selected for sequencing. It corresponds to
 a full length, in-frame gamma T cell antigen receptor transcript.
 CC (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
 CC to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 1080 BP; 324 A; 257 C; 233 G; 266 T; 0 U; 0 Other;
 DR Alignment Scores:
 Pred. No.: 1.63e-29 Length: 1080
 Score: 279.00 Matches: 53
 Percent Similarity: 96.55% Conservative: 3
 Best Local Similarity: 91.38% Mismatches: 2
 Query Match: 90.88% Indels: 0
 DB Gaps: 0
 DR:
 US-10-031-158-14 (1-58) x AAN91698 (1-1080)
 QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
 DR 452 ATCCAGAGTGTTCCTCCAGCCACTTTCTCTCGATGCGAACAACTCC 511
 QY 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyr 40
 DR 512 AGAAGGCTGGACATCTTCTGAGAAATTTCAGATATTCCAGGAGATTATAAGTAG 571
 RESULT 31 ABV37836
 ID ABV37856 standard; cDNA; 533 BP.
 XX AC ABV37856;
 XX DT 16-SEP-2002 (first entry)
 XX DB Human prostate expression marker cDNA 37847.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX OS Homo sapiens.
 XX PN WO20010860-A2.
 XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US005171.
 XX PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endge WO, Monahan JE;
 XX DR

PA (HUMAN GENOME SCI INC.
 ROSE/) ROSEN C A.
 PT Rosen CA, Ruben SM;
 XX WPI; 2000-587513/55.
 DR P-PSDB; AAB56420.

XX Prostate cancer associated gene sequences, referred to as prostate cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PR such as prostate cancer.

XX Claim 1; Page 655-656; 2338pp; English.

XX AAF1556 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB5633 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardiotropic, immunomodulatory, pulmonary, gastrointestinal,
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polymucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 1155 BP; 359 A; 242 C; 225 G; 317 T; 0 U; 12 Other;

XX Alignment Scores:
 Pred. No.: 1.21e-24 Length: 1155
 Score: 245.00 Matches: 51
 Percent Similarity: 91.07% Conservative: 0
 Best Local Similarity: 91.07% Mismatches: 5
 Query Match: 79.80% Indels: 1
 DB: 3 Gaps: 0

US-10-031-158-14 (1-58) x AAF15623 (1-1155)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGinSerSer 20
 Db 175 ATGCAGATGTTCCCCAACGCCACTATT-TTCTCTTCRATGCTGAACAACTCC 233

QY 21 ArgArgLeuGluIleThrPheValPheLeuIysGlnPheSerLeuMetLeuLeuArgTyr 40
 Db 234 AGAAGGCTGGAACTACCTTGCTCTGAGAAATTTCCTGAGATTAAGATACT 293

QY 41 IleGlyLysIysArgArgAlaThrArgPheTrpAspProArgArgGly 56
 Db 294 ATGGGSAAGAAGAGAGCAACAGGATCTGGATCCAGGGGG 341

RESULT 34 ABV29989/c

ID ABV29989 standard; cDNA; 1022 BP.

XX ABV29989;
 XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 29980.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PT Schlegel R, Endege WO, Monahan JE;
 PR WPI; 2001-662795/76.

XX DR Novel isolated nucleic acid molecule associated with cancerous state of
 CC prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 6477; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification of its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 1022 BP; 288 A; 203 C; 220 G; 311 T; 0 U; 0 Other;

XX SQ Alignment Scores:
 Pred. No.: 5.29e-24 Length: 1022
 Score: 200.00 Matches: 47
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 97.92% Mismatches: 0
 Query Match: 78.18% Indels: 0
 DB: 5 Gaps: 0

US-10-031-158-14 (1-58) x ABV29989 (1-1022)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGinSerSer 20
 Db 589 ATGCAGATGTTCCCCAACGCCACTATT-TTCTCTTCRATGCTGAACAACTCC 530

QY 21 ArgArgLeuGluIleThrPheValPheLeuIysGlnPheSerLeuMetLeuLeuArgTyr 40
 Db 529 AGAAGGCTGGAACTACCTTGCTCTGAGAAATTTCCTGAGATTAAGATACT 470

QY 41 IleGlyLysIysArgArgAlaThrArgPheTrpAspProArgArgGly 48
 DB: 469 ATGGGAAAGAAGAGAGCATCG 446

RESULT 35 ABV24072/c

ID ABV24072 standard; cDNA; 1022 BP.

XX AC ABV24072;
 XX DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 24063.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

DE Human prostate expression marker cDNA 25514.
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX WO200160860-A2.
 PD 23-AUG-2001.
 XX PR 20-FEB-2001; 2001WO-US005171.
 XX PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 01-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX PS Claim 1; Page 5198; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV6213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 CC Sequence 1022 BP; 288 A; 203 C; 220 G; 311 T; 0 U; 0 Other;
 CC Alignment Scores:
 CC Pred. No.: 5.29e-24 Length: 1022
 CC Score: 240.00 Matches: 47
 CC Percent Similarity: 100.00% Conservative: 1
 CC Best Local Similarity: 97.92% Mismatches: 0
 CC Query Match: 78.18% Indels: 0
 CC DB: 5 Gaps: 0
 US-10-031-158-14 (1-58) x ABV25823 (1-1022)
 QY 1 MetGlnMetpheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 DB 589 ATGCAGATGTTTCCCCAACCCACTATTTCCTCTCTGAAATTTCCTGATGTATTAGATAAC 530
 QY 21 ArgArgLeuGluLysThrPheValPheLeuGlnPheSerLeuMetLeuLeuArgTrp 40
 DB 529 AGAAGCTGGAAACATACCTTGCTCTGAGAAATTTCCTGATGTATTAGATAAC 470
 QY 41 IleGlyLysLysSarGargAlaThr 48
 DB 469 ATTGGGAGAGAAAGAGAGCATCG 446
 RESULT 38 ABV24034/C ID ABV24034 standard; cDNA; 1022 BP.
 XX

AC ABV24034;
 XX DT 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 24025.
 DE Human prostate expression marker cDNA 24025.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 XX Pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX PR WO200160860-A2.
 XX PR 20-FEB-2001; 2001WO-US005171.
 XX PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, stage of prostate cancer.
 XX PS Claim 1; Page 4456; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV6213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 CC Sequence 1022 BP; 288 A; 203 C; 220 G; 311 T; 0 U; 0 Other;
 CC Alignment Scores:
 CC Pred. No.: 5.29e-24 Length: 1022
 CC Score: 240.00 Matches: 47
 CC Percent Similarity: 100.00% Conservative: 1
 CC Best Local Similarity: 97.92% Mismatches: 0
 CC Query Match: 78.18% Indels: 0
 CC DB: 5 Gaps: 0
 US-10-031-158-14 (1-58) x ABV24034 (1-1022)
 QY 1 MetGlnMetpheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 DB 589 ATGCAGATGTTTCCCCAACCCACTATTTCCTCTCTGAAATTTCCTGATGTATTAGATAAC 530
 QY 21 ArgArgLeuGluLysThrPheValPheLeuGlnPheSerLeuMetLeuLeuArgTrp 40
 DB 529 AGAAGCTGGAAACATACCTTGCTCTGAGAAATTTCCTGATGTATTAGATAAC 470
 QY 41 IleGlyLysLysSarGargAlaThr 48
 DB 469 ATTGGGAGAGAAAGAGAGCATCG 446

RESULT 39
ABV23986/c
ID ABV23986 standard; cDNA: 1022 BP.
XX

AC ABV23986;
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23977.
XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.
XX

OS Homo sapiens.
XX

PN WO200160860-A2.
XX

PD 23-AUG-2001.
XX

PP 20-FEB-2001; 2001WO-US005171.
XX

PR 17-FEB-2000; 2000US-0183319P.
XX

PR 16-MAR-2000; 2000US-0189862P.
XX

PR 25-MAY-2000; 2000US-0207454P.
XX

PR 09-JUN-2000; 2000US-0211314P.
XX

PR 18-JUL-2000; 2000US-0219007P.
XX

PR 13-DEC-2000; 2000US-0255281P.
XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX

PT Schlegel R, Endge WO, Monahan JE;
DR XX

PT WPI; 2001-662795/76.
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
XX

PS Claim 1; Page 4439; 11750pp; English.
XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX

SQ Sequence 1022 BP; 288 A; 203 C; 220 G; 311 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5.29e-24 Length: 1022
Score: 240.00 Matches: 47
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 97.92% Mismatches: 0
Query Match: 5 Indels: 0
Gaps: 0
US-10-031-158-14 (1-58) x ABV23986 (1-1022)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIleGlnSer 20
Db 589 ATGCAGATGTTCGCCAAGCCACTATTTCTCTCAATGCGAAATTTTCCGTGATTTAAGATAC 530

RESULT 40
ABV23991/c
ID ABV23991 Standard; cDNA: 1022 BP.
XX

AC ABV23991;
DT 16-SEP-2002 (first entry)
XX

DE Human prostate expression marker cDNA 23982.
XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.
XX

OS Homo sapiens.
XX

PN WO200160860-A2.
XX

PD 23-AUG-2001.
XX

PP 20-FEB-2001; 2001WO-US005171.
XX

PR 17-FEB-2000; 2000US-0183319P.
XX

PR 16-MAR-2000; 2000US-0189862P.
XX

PR 25-MAY-2000; 2000US-0207454P.
XX

PR 09-JUN-2000; 2000US-0211314P.
XX

PR 18-JUL-2000; 2000US-0219007P.
XX

PR 13-DEC-2000; 2000US-0255281P.
XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX

PT Schlegel R, Endge WO, Monahan JE;
DR XX

PT WPI; 2001-662795/76.
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
XX

PS Claim 1; Page 4442; 11750pp; English.
XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
CC
XX

SQ Sequence 1022 BP; 288 A; 203 C; 220 G; 311 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5.29e-24 Length: 1022
Score: 240.00 Matches: 47
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 97.92% Mismatches: 0
Query Match: 5 Indels: 0
Gaps: 0
US-10-031-158-14 (1-58) x ABV23991 (1-1022)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIleGlnSer 20
Db 589 ATGCAGATGTTCGCCAAGCCACTATTTCTCTCAATGCGAAATTTTCCGTGATTTAAGATAC 530

QY 21 ArgArgLeuGluLysThrPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
Db 529 AGAGGCTGGAAATACCTTGCTTCCTGAGAAATTTCCTGATGTTAAGATA 470
QY 41 IleGlyLysLysArgArgAlaThr 48
Db 469 ATGGGAGAAGAGAGGATCG 446

Search completed: December 8, 2004, 08:22:18
Job time : 253 secs

/lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="N1H_MGC_83"

/notes="organ: prostate; Vector: pDNR-LIB (Clontech);

Site_1: SfiI (ggccgcctggcc); Site_2: SfiI
 (ggccatccatggcc); 5' and 3' adaptors were used in cloning,
 as follows: 5' adaptor sequence: 5'-CACGCCATATGGCC-3',
 and 3' adaptor sequence: 5'-ATTCTAGGGGAGGGGACATG-3' (where B = A,
 C', or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Alignment Scores:
 Pred. No.: 1.17e-30 Length: 427
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-031-158-14 (1-58) x BF679325 (1-427)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20

Db 66 ATGCAGATGTTCGCCAACCCACTATTTCCTCTCAATTGCTGAAACAAGCTCC 125

Qy 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40

Db 126 AGAGGCTGGACATCTTGCTCTGAGAAATTTCCTGAGTGTATTAGATAC 185

Qy 41 IleGlyIysLysBsaRgRgAthrArgPhePaspProArgPhePaspProArgGlyThrPro 58

Db 186 ATTCGGAGAGAGAGAGAGCAGCACCATCTGGATGCCAGGGGAAACCCA 239

RESULT 2

AV716204 AV716204 510 bp mRNA linear EST 11-OCT-2000

DEFINITION AV716204 DCB Homo sapiens cDNA clone DCBAM008 5', mRNA sequence.

ACCESSION AV716204 VERSION AV716204.1 KEYWORDS EST.

SOURCE ORGANISM Homo sapiens (human)

REFERENCE AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

LOCUS LOCUS AV715641 DCB Homo sapiens cDNA clone DCBBSB05 5', mRNA sequence.

COMMENT TITLE JOURNAL CONTACT Unpublished (2000)

AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

VERSION VERSION AV715641.1 KEYWORDS GI:10797158

TITLE JOURNAL COMMENT CONTACT Unpublished (2000)

KEYWORDS EST.

TITLE JOURNAL COMMENT CONTACT Unpublished (2000)

KEYWORDS TITLE JOURNAL COMMENT CONTACT Unpublished (2000)

REFERENCE AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

TITLE JOURNAL COMMENT CONTACT Unpublished (2000)

REFERENCE AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

COMMENT TITLE JOURNAL COMMENT CONTACT Unpublished (2000)

FEATURES SOURCE

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-30 Length: 510
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

/note="Vector: pTRIPEx2; Site_1: SfIA; Site_2: SfIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.74e-30 Length: 596
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV715641 (1-596)

Qy 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db 93 ATCCAGATGTTCCCCAACGCCACTTTCCTCTCAATTGCTGAACAAAGCTCC 152
 Qy 21 ArgArgLeuGluHistPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
 Db 153 AGAGGGCTGGAACATACTTCTGCTCTGAGAAATTTCCTGATGTATTAAGATAC 212
 Qy 41 IleGlyLysIleSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 213 ATGGCAAGAAGAAGAAGGACACAGATCTGGATCCAGGGGACACCA 266

RESULT 4
 AV714189
 LOCUS AV714189 mRNA linear EST 11-OCT-2000
 DEFINITION AV714189 DBC Homo sapiens cDNA clone DCBBQE09 5', mRNA sequence.
 ACCESSION AV714189
 VERSION AV714189.1 GI:10914340
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 803)
 AUTHORS Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
 Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
 Song,H., Gu,Y., Yang,Y., Gao,X., Xiao,H., Li,N., Qian,B., Gao,X.,
 Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
 Lu,G., Cheng,Z. and Han,Z.
 TITLE Homo sapiens
 JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 COMMENT Unpublished (2000)
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES source
 1. . .803
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone "BMRBAF12"
 /tissue_type="Bone marrow"
 /cell_type="CD4+ hematopoietic stem/progenitor cell"
 /lab_host="BM25.8"
 /clone_id="BM"
 /note="Vector: pTripleX2; Site_1: sfIIA; Site_2: sfIIB"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.48e-30 Length: 803
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV714189 (1-603)

Qy 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db 434 ATCCAGATGTTCCCCAACGCCACTTTCCTCTCAATTGCTGAACAAAGCTCC 493
 Qy 21 ArgArgLeuGluHistPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
 Db 494 AGAGGGCTGGAACATACTTCTGCTCTGAGAAATTTCCTGATGTATTAAGATAC 553
 Qy 41 IleGlyLysIleSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 554 ATGGCAAGAAGAAGGACACAGATCTGGATCCAGGGGACACCA 607

RESULT 5
 AV756492
 LOCUS AV756492 mRNA linear EST 19-OCT-2000
 DEFINITION AV756492 BM Homo sapiens cDNA clone BMRBAF12 5', mRNA sequence.
 ACCESSION AV756492.1 GI:10914340
 VERSION EST.
 KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 803)
 AUTHORS Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
 Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
 Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Pu,G., Ren,S., Zhong,M.,
 Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and
 Chen,Z.
 TITLE Homo sapiens cDNA BM clones
 JOURNAL Unpublished (2000)
 COMMENT Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES source
 1. . .803
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone "BMRBAF12"
 /tissue_type="Bone marrow"
 /cell_type="CD4+ hematopoietic stem/progenitor cell"
 /lab_host="BM25.8"
 /clone_id="BM"
 /note="Vector: pTripleX2; Site_1: sfIIA; Site_2: sfIIB"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.48e-30 Length: 803
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-031-158-14 (1-58) x AV756492 (1-803)

Qy 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db 21 ArgArgLeuGluHistPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
 Qy 22 ArgArgLeuGluHistPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
 Db 312 AGAAGGCTGGAACATACTTCTGCTCTGAGAAATTTCCTGATGTATTAAGATAC 371
 Qy 41 IleGlyLysIleSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
 Db 372 ATTCGCAAGAAGAAGGACACAGATCTGGATCCAGGGGACACCA 425

		TITLE JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
REFERENCE	COMMENT	Unpublished (1999)	Contact: Robert Strausberg, Ph.D.
AUTHORS	COMMENT	Email: cgabbs@mail.nih.gov	Tissue Procurement: Life Technologies, Inc.
JOURNAL	COMMENT		CDNA Library Preparation: CLONTECH Laboratories, Inc.
COMMENT			CDNA Library Preparation: CLONETECH Laboratories, Inc.
CONTACT			CDNA Sequencing by: Incyte Genomics, Inc.
EMAIL			Clone distribution by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
URL			Plate: LLNL11524 row: e column: 10
CDNA LIBRARY PREPARATION			High quality sequence stop: 816.
CDNA SEQUENCING			Location/Qualifiers
COMMENT			1. .818
COMMENT			/organism="Homo sapiens"
COMMENT			/mol_type="mRNA"
COMMENT			/db_xref="taxon:606"
COMMENT			/clone="IMAGE:5208945"
COMMENT			/lab_host="DH10B"
COMMENT			/clone lib="NIH MGC 122"
COMMENT			/note="Organ: pooled lung and spleen; vector: pCMV-SPOR16;
COMMENT			Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note:
FEATURES	Source	ORIGIN	this is a NIH_MGC Library."
COMMENT			Alignment Scores:
PREDICTION	Pred. No.:	Length:	818
SCORE	Score: 307.00	Matches:	58
PERCENT SIMILARITY	Percent Similarity: 100.00%	Conservative:	0
BEST LOCAL SIMILARITY	Best Local Similarity: 100.00%	Mismatches:	0
QUERY MATCH	Query Match: 100.00%	Indels:	0
DB:	Gaps: 4		
US-10-031-158-14 (1-58) x BI771070 (1-818)			
QY	1 MetGlnMetPheProProSerProleuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20	Alignment Scores:	2.5546-30
DB	548 ATGCAGATGTTCCTCCAAAGCCCACTATTTCCTCTCAATTGCTGAACAAAGCTCC 607	Pred. No.:	307.00
QY	21 ArgArgLeuGluIleThrPheValPheLeuArgGlnPheSerSerIleLeuLeuArgTyr 40	Length:	818
DB	608 AGAACGCTGGCACATCTTGCTCTTGAGAATTTCCCTGATGTATAGATAC 667	Score:	307.00
QY	41 IleGlyIleIysArgArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58	Percent Similarity:	100.00%
DB	668 ATTGCCAAGAAAGAGCACACGATCCTGGATCCAGGGAAACACCA 721	Best Local Similarity:	100.00%
RESULT	7	Query Match:	2
LOCUS	BF679123	DB:	64 ATGCAGATGTTCCTCCAAAGCCCACTATTTCCTCTCAATTGCTGAACAAAGCTCC 123
DEFINITION	BF679123 821 bp mRNA linear EST 21-DEC-2000	QY	21 ArgArgLeuGluIleThrPheValPheLeuArgGlnPheSerSerIleLeuLeuArgTyr 40
ACCESSION	60215390F1 NIH_MGC_B3 Homo sapiens CDNA clone IMAGE:4294275', mRNA sequence.	DB	124 AGAGGCTGCAACTTACCTTGCTCTTGAGAATTTCCCTGATGTATAGATAC 183
VERSION	BF679123	QY	41 IleGlyIleIysArgArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58
KEYWORDS	EST.	DB	184 ATTGGCAAGAAAGAGCACACGATCTGGATCCAGGGAGGACACCA 237
SOURCE	Homo sapiens (human)	RESULT	8
ORGANISM	Homo sapiens	DEFINITION	BF681385 861 bp mRNA linear EST 21-DEC-2000
REFERENCE		ACCESSION	602156579F1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4297555', mRNA sequence.
AUTHORS		VERSION	BF681385.1 GI:11955280
JOURNAL		KEYWORDS	Homo sapiens (human)
COMMENT		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 861)	REFERENCE	1 NIH-MGC http://mgc.nci.nih.gov/
AUTHORS	1 (bases 1 to 821)	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/	COMMENT	Unpublished (1999)
AUTHORS		COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics Inc.

Clone distribution by: Incyte Genomics Inc.

Clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LUCM151 row: n column: 20

High quality sequence stop: 672.

FEATURES

source
 Location/Qualifiers
 1 . 861
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4297555"
 /lab host="DH10B (T1 phage-resistant)"
 /clone lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SFI1 (ggccgcgttcgcc); Site 2: SFI1
 (ggccattatggcc); 5', and 3', adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'
 and 3' adaptor sequence:
 5'-ATCTAGAGGCCAGGCGCCGACATG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 1415 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

FEATURES

source

Location/Qualifiers

1 . 865

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 866

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 866

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

Location/Qualifiers

1 . 867

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone lib="tumor2"

/note="Organ: prostate; Vector: pBluescript; Directional
 CDNA library was constructed using Lambda ZP II kit
 (Stratagene). mRNA was extracted from a frozen prostate
 tumor tissue (Mayo Clinics)."

FEATURES

source

/lab_host="DH10B (T1 Phage-resistant)"
/clone_lib="NIH_MGC_83"
/note=Organ: prostate; Vector: pDNR-LIB (Clontech);
site 1: SfiI (ggccgcctcgcc); Site 2: SfiI
(ggcattatggcc); 5', adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'
and 3' adaptor sequence: 5'-ATTCTAGGGCCAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN

Alignment Scores:
Pred. No.: 2.77e-30 Length: 891
Score: 307.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2 Index: 0
DB: Gaps: 0

US-10-031-158-14 (1-58) x BF677648 (1-881)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
64 ATGCAGATGTTCGCCAACGCCCACATTTCCTCTCATGCTGAAACAAGCTCC 123
21 ArgArgLeuGluHisThrPheValPheLeuArgGlnPheSerLeuLeuMetLeuLeuArgTrp 40
124 AGAAGGCTGGAACATACCTTGCTCTGAGAAATTTCCTGATGTATTAGATAC 183
Qy 41 IleGlyLysSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
184 ATTGGCGAAGAAGAAGAAGGAGCAGCATGTTGGATCCCGAGGGAGCACCA 237

RESULT 11

BF674593 LOCUS BF674593 902 bp mRNA linear EST 21-DEC-2000
DEFINITION 60213761P1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274283 5',
mRNA sequence.

ACCESSION BF674593
VERSION BF674593.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Burkittya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 902)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rsrmail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
DNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LCM101 row: e column: 04
High quality sequence stop: 629.

FEATURES source
Location/Qualifiers

1. 902
Organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4274507"
/lab_host="DH10B (T1 Phage-resistant)"

/clone_lib="NIH_MGC_83"
note=Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgcctcgcc); Site 2: SfiI
(ggcattatggcc); 5', adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'

/note=Organ: prostate; Vector: pDNR-LIB (Clontech);
/clone_lib="NIH_MGC_83"
/note=Organ: prostate; Vector: pDNR-LIB (Clontech);

ORIGIN

Alignment Scores:
Pred. No.: 2.85e-30 Length: 902
Score: 307.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2 Index: 0
DB: Gaps: 0

US-10-031-158-14 (1-58) x BR674593 (1-902)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
64 ATGCAGATGTTCGCCAACGCCCACATTTCCTCTCATGCTGAAACAAGCTCC 123
21 ArgArgLeuGluHisThrPheValPheLeuArgGlnPheSerLeuLeuMetLeuLeuArgTrp 40
124 AGAAGGCTGGAACATACCTTGCTCTGAGAAATTTCCTGATGTATTAGATAC 183
Qy 41 IleGlyLysSarGargAlaThrArgPheTrpAspProArgArgGlyThrPro 58
184 ATTGGCGAAGAAGAAGGAGCAGCATGTTGGATCCCGAGGGAGCACCA 237

RESULT 12

BR679476 LOCUS BR679476 927 bp mRNA linear EST 21-DEC-2000
DEFINITION 60215280P1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294507 5',
mRNA sequence.

ACCESSION BR679476
VERSION BR679476.1
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Burkittya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 927)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rsrmail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
DNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LCM1143 row: o column: 20
High quality sequence stop: 573.

FEATURES source
Location/Qualifiers

1. 927
Organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294507"
/lab_host="DH10B (T1 Phage-resistant)"

/clone_lib="NIH_MGC_83"
note=Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgcctcgcc); Site 2: SfiI
(ggcattatggcc); 5', adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'

/note=Organ: prostate; Vector: pDNR-LIB (Clontech);
/clone_lib="NIH_MGC_83"
/note=Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgcctcgcc); Site 2: SfiI
(ggcattatggcc); 5', adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'
and 3' adaptor sequence:
5'-ATTCAGGGCCAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

and 3' adapter sequence:
 5'-ATCTAGAGCCGAGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).

ORIGIN

Alignment Scores:
Pred. No.: 2.94e-30 **Length:** 927
Score: 307.00 **Matches:** 58
Percent Similarity: 100.00% **Conservative:** 0
Best Local Similarity: 100.00% **Mismatches:** 0
Query Match: 100.00% **Indels:** 0
DB: 2 **Gaps:** 0

US-10-031-158-14 (1-58) x BR679476 (1-927)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnIleLeuLeuLysGinSerSer 20

Db 67 ATGGAGATGTCCCCAACGCCACTATTTCTTCCTCAATGCTGAAAGCTC 126

QY 21 ArgArgLeuGluHisThrRheValPheLeuArgPheSerIleMetLeuLeuArgTyr 40

Db 127 AGAAGGCTGGACACATACCTTGCTCTGAGAAATTTCCTGTATGTTAGATA 186

QY 41 IleGlyLysLysSarGargAlaThrArgPheTerPheProArgGlyIlePro 58

Db 187 ATTGGCAAGAAAGAGCACACGATCTGGAATCCAGGAGGGACACCA 240

RESULT 13

BM544213

LOCUS BM544213 1058 bp mRNA linear EST 20-FEB-2002

DEFINITION AGENCOURT 6490556 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587705

ACCESSION 5', mRNA sequence.

VERSION BM544213.1

TITLE GI:18775279

KEYWORDS EST,

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

Mammal;

Bacteria;

Primates;

Catarrhini;

Hominidae;

Homo.

AUTHORS

NIH-MGC

http://mgc.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: gamps-r@mail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LIAM12357 row: k column: 02

High quality sequence start: 12

High quality sequence stop: 768.

FEATURES

source

Location/Qualifiers

1. .1058

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:606"

/clone="IMAGE:5587705"

/lab_host="Dilbo"

/clone.lib="NIH_MGC_125"

/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;

Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool

of three ovaries, from females ranging in age from 38 to

49 yo. Library is oligo dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 2.1 kb, insert size range 1-3.5 kb. Library is

normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036. "C" stands for Clontech.

ORIGIN

Alignment Scores:
Pred. No.: 3.44e-30 **Length:** 1058
Score: 307.00 **Matches:** 58
Percent Similarity: 100.00% **Conservative:** 0
Best Local Similarity: 100.00% **Mismatches:** 0
Query Match: 100.00% **Indels:** 0
DB: 4 **Gaps:** 0

US-10-031-158-14 (1-58) x BM544213 (1-1058)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnIleLeuLeuLysGinSerSer 20

Db 421 ATGGAGATGTCCCCAACGCCACTATTTCTTCCTCAATGCTGAAACAGCTC 480

QY 21 ArgArgLeuGluHisThrRheValPheLeuArgPheSerIleMetLeuLeuArgTyr 40

Db 481 AGAGGCGGAGACATACCTTGCTCTGAAATTTCCTGATGTTAAGATAAC 540

QY 41 IleGlyLysLysSarGargAlaThrArgPheTerPheProArgArgGlyIlePro 58

Db 541 ATGGCAGAAGAGAGCACACGATCTGGATCCAGGAGGGACACCA 594

RESULT 14

BC030554

DEFINITION

BC030554

LOCUS BC030554

VERSION BC030554.1

TITLE GI:20980582

KEYWORDS HIC.

REFERENCE

1 (bases 1 to 3533)

AUTHORS

Strausberg, R.

TITLE

Submitted (07-MAY-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

Contact: NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT

Contact: MGC help desk

Email: gamps-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Contact: nisc_mgc@nigri.nih.gov

Akher, N., Ayotte, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.J., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hachighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Lalic, P., Legaspi, R., Maduro, O.L.,

Masliallo, C., Maskeri, B., Mastriani, S.D., McCloskey, J.C., McDowell, J.J.,

Pearson, R., Stantrup, S., Thomas, P.J., Touchman, J.W., Tautz, D.,

Vogt, J.L., Walter, M.A., Wetherby, K.D., Wiggins, L., Young, A.,

Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: INRA Plate: 64 Row: k Column: 18

This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers

1. .3533

/organism="Homo sapiens"

Alignment Scores: 1.44e-29 Length: 3533
 Pred. No.: 307.00 Matches: 58
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indexes: 0
 Query Match: 3 Gaps: 0

ORIGIN

Alignment Scores: 1.44e-29 Length: 3533
 Pred. No.: 307.00 Matches: 58
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indexes: 0
 Query Match: 3 Gaps: 0

US-10-031-158-14 (1-58) x BU199143 (1-3533)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuLysGlnSerSer 20
 Db 758 ATGCAGATGTTCCCCAACCCACTATTTCCTCTCAATGCTGAAACAAGCTCC 817

Qy 21 ArgArgLeuGluHisthRheValPheLeuArgAanPhsSerLeuMetLeuLeuArgTyr 40
 Db 818 AGAGGCTGGACACACTTGCTCTTGAAGATTTCCTGTGAGATTTAGATAC 877

Qy 41 IleGlyLysIysSargArgAlaThrArgPheAspProArgArgLysThrPro 58
 Db 878 ATTCGCGAGAGAGAGAGACAGATTCGGATCCAGGAGGGAGACCA 931

RESULT 15

BU199143 Locus BU199143 Definition 739 bp mRNA linear EST 05-SBP-2002
 DEFINITION DBTcia08 DCB Homo sapiens cDNA, mRNA sequence.
 ACCESSION BU199143
 VERSION BU199143.1 GI:22717723
 KEYWORDS EST.

SOURCE ORGANISM Homo sapiens (human)

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Bulykova; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgbps-1@mail.nih.gov

FEATURES Source

PLATE: LICM817 row: 1 column: 05
 High quality sequence stop: 651.
 Location/Qualifiers 1..653

TITLE JOURNAL
 COMMENT Unpublished (2000)
 Contact: Zengang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 Tel: 86-21-5801919 (ex:45)
 Fax: 86-21-5801922
 Email: hanzg@chgc.sh.cn

FEATURES source
 Location/Qualifiers 1..789

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /mol_type="mRNA"
 /cell_type="dendritic cells"
 /dev_Stage="mature"
 /lab_host="BMS5.8"
 /clone_lib="DBB"
 /note="vector: pTRIPLEX2; site_1: SfIIA; site_2: SfIIB"

ORIGIN

Alignment Scores: 1.00e-28 Length: 653
 Pred. No.: 294.00 Matches: 58
 Score: 98.31% Conservative: 0
 Percent Similarity: 98.31% Mismatches: 0
 Best Local Similarity: 95.77% Indexes: 1
 Query Match: 2 Gaps: 0

Qy Match: 99.02% Indexes: 0
 DB: Gaps: 0

US-10-031-158-14 (1-58) x BU199143 (1-789)

Qy 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
 Db 119 ATGGAGAGTTCCCCAACCCACTATTTCCTGTGAAACAAGCTCC 178

Qy 21 ArgArgLeuGluHisthRheValPheLeuArgAanPhsSerLeuMetLeuLeuArgTyr 40
 Db 179 AGAGGCTGGACACACTTGCTCTTGAAGATTTCCTGTGAGATTTAGATAC 238

Qy 41 IleGlyLysIysSargArgAlaThrArgPheAspProArgArgLysThrPro 58
 Db 239 ATTGGCAAGAAAGAGCACACGATTCCTGGATCCAGGAGGGAGACCA 292

RESULT 16

BE974171 Locus BE974171 Definition 601680522F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950740 5,
 DEFINITION mRNA sequence.
 ACCESSION BE974171
 VERSION BE974171.1 GI:10587507
 KEYWORDS EST.

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Bulykova; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgbps-1@mail.nih.gov

FEATURES Source

PLATE: LICM817 row: 1 column: 05
 High quality sequence stop: 651.
 Location/Qualifiers 1..653

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="DBB"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: SfII (ggcccttgcggcc); Site_2: SfII
 (ggccatattggcc); 5' and 3' adaptors were used in cloning,
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3',
 and 3' adaptor sequence: 5'-ATTCAGGCCGGCCGACATG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Alignment Scores: 1.00e-28 Length: 653
 Pred. No.: 294.00 Matches: 58
 Score: 98.31% Conservative: 0
 Percent Similarity: 98.31% Mismatches: 0
 Best Local Similarity: 95.77% Indexes: 1
 Query Match: 2 Gaps: 0

US-10-031-158-14 (1-58) x BB974171 (1-653)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuIysGlnSerSer 20
Db 310 ATGCAGATGTTCCCCAACGCCACTATTTCCTCTCAATGCTGAACAAAGCTC 369

QY 21 ArgArgLeuGluLisThrPheValPheLeuArgAsnDheSerLeuMetLeuLeuArgTyr 40
Db 457 AGAGGCTGGAGATACTCTTGCTCTGAGAAATTTCCTGATTTATTAAGATAC 516

QY 41 IleGlyLysIysArgArgAlaThrArgPhePheTrpAspProArgArgGlyThrPro 58
Db 370 AGAGGCTGGAGACATACTCTGCTCTGATGTTAAGATA 429

QY 41 Ile-Gly-Lys-Iys-Sarg-Arg-Gal-thr-Ara-Arg-Phe-Trp-Asp-Pro-Arg-Gly-Thr-Pro 58
Db 430 ATTGGCAGAAGAACACGATTCGGCATCCGGAGGGGACACCA 484

RESULT 17
Bm919380 BM919380 1005 bp mRNA linear EST 12-MAR-2002

DEFINITION AGENCOURT 671566 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:574632

ACCESSION BM919380
VERSION BM919380.1 GI:19369759

AUTHORS EST:
KEYWORDS SOURCE
ORGANISM Homo sapiens (human)
COMMENT
Email: cgabbs@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:
http://image.llnl.gov
Plate: LILNL2776 row: 1 column: 09

High quality sequence stop: 609.

FEATURES source
1. .105
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5748632"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ_pooled pancreas and spleen; Vector:
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5748632"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ_pooled pancreas and spleen; Vector:
/mol_type="mRNA"
source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 1.76e-28 Length: 1005 Matches: 55 Conservative: 2 Mismatches: 1
Percent Similarity: 98.28% Best Local Similarity: 94.83% Query Match: 95.77%
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x BM919380 (1-1005)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuIysGlnSerSer 20
Db 397 ATGCAGATGTTCCCCAACGCCACTATTTCCTCTCAATGCTGAACAAACTCC 756

QY 21 ArgArgLeuGluLisThrPheValPheLeuArgAsnDheSerLeuMetLeuLeuArgTyr 40
Db 457 AGAGGCTGGAGATACTCTTGCTCTGAGAAATTTCCTGATTTATTAAGATAC 516

QY 41 IleGlyLysIysArgArgAlaThrArgPhePheTrpAspProArgArgGlyThrPro 58
Db 517 ATTGGCAGAAGAACACGATTCGGCATCCGGAGGGGACACCA 570

RESULT 18
Bc039116 BC039116 1757 bp mRNA linear HTC 04-MAR-2003

DEFINITION Homo Sapiens, Similar to T-cell receptor gamma, constant 2, clone IMAGE:4829750, mRNA.

ACCESSION BC039116
VERSION BC039116.1 GI:25056606

REFERENCE 1 (bases 1 to 1757)

AUTHORS HRC.
TITLE Homo sapiens (human)
COMMENT Direct Submission
Email: cgabbs@mail.nih.gov
Tissue Procurement: Miklos Rakovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BOM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contract: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Rakovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BOM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Guneratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisegard, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov Series: LILNL Plate: 72 Row: F Column: 5 This clone has the following problem: retained intron.

FEATURES source
1. .157
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:829750"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN
Alignment Scores:
Pred. No.: 3.41e-28 Length: 1757 Matches: 55 Conservative: 2 Mismatches: 1
Score: 294.00 Best Local Similarity: 98.28% Query Match: 95.77%
Percent Similarity: 98.28% Indels: 0
DB: 3 Gaps: 0

US-10-031-158-14 (1-58) x BC039116 (1-1757)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuIysGlnSerSer 20
Db 700 ATGCAGATGTTCCCCAACGCCACTATTTCCTCTCAATGCTGAACAACTCC 759

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgPheSerLeuMetLeuLeuArgTyr 40
 Db 760 AGAAGGCTGCAACATACTTGTCCTCTGAAATTTCAGATATTAAAGATAC 819

QY 41 IleGlyLysSlysArgArgAlaThrArgPheTerPheProArgArgGlyThrPro 58
 Db 820 ATGGCCAGAAAGAAGAGGACACGATCTGGATCCCGAGGGAAACCCA 873

RESULT 19
 LOCUS BPF47659/c
 DEFINITION QV2-BT0616-051200-521-c07 BT0616 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF747659
 VERSION BF747659.1 GI:12074335

KEYWORDS EST,
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 434)

REFERENCE 1
 AUTHORS Dias Neto,B Garcia Correa,R., Veriovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W.J., Zogo,M.A., Bordim,S., Costa,F.F.,
 Goldmann,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Ribeiro,L.P., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
 PUBMED 20202663
 COMMENT Contact: Simpson A.J.G.
 Ludwig Institute for Cancer Research
 Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.qc.br/scripts/gethtml2.p1?t1=QV2&t2=QV2-BT0616-051200-521-c07&t3=2001-12-05&t4=1>)

Seq primer: puc 18 forward
 High quality sequence start: 21
 High quality sequence stop: 320.
 Location/Qualifiers

1. .434
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2581344"
 /lab_host="DH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /notes="Organ: pooled; Vector: PT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBL19W, testis NHR, and B-cell
 NCI CGAP GCB) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 29480-302087, 685632-687239,
 726408-728711, and 728096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

FEATURES source

1. .497
 /location/Qualifiers
 1. .497
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_idb="BT0616"
 /note="Organ: breast; Vector: pUC18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 2.22e-28 Length: 434
 Score: 290.00 Matches: 54
 Percent Similarity: 98.28% Conservative: 3
 Best Local Similarity: 93.10% Mismatches: 1
 Query Match: 94.46% Indels: 0
 DB: 2 Gaps: 0

US-10-031-158-14 (1-58) x AW087486 (1-497)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuArgGlnSerSer 20
 Db 305 ATGCAGATTTTCGCCAGCCACTATTTCTCCTGATGCTAACAACTCC 246

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgPheSerLeuMetLeuLeuArgTyr 40
 Db 245 AGAAGGCTGGAACATACCTTGTCTCTGAGAATTTCAGATATTAAAGATAC 186

QY 41 IleGlyLysSlysArgArgAlaThrArgPheTerPheProArgArgGlyThrPro 58
 Db 185 ATGGCCAGAAAGAAGAGGACACGATCTGGATCCAGGGAAACCCA 132

RESULT 20
 LOCUS AW087486
 DEFINITION XB67501.x1l Soares NFL T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2581344 3' similar to gb:MI3231 T-CELL RECEPTOR GAMMA CHAIN C
 REGION (HUMAN); mRNA sequence.

KEYWORDS EST,
 SOURCE Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 497)

REFERENCE 1
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT Contact: Robert Strasberg, Ph.D.
 Email: cgbps@mail.nih.gov
 This clone is available royalty-free through LILN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -40UP from Gibco
 High quality sequence stop: 415.
 Location/Qualifiers

1. .497
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2581344"
 /lab_host="DH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /notes="Organ: pooled; Vector: PT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBL19W, testis NHR, and B-cell
 NCI CGAP GCB) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 29480-302087, 685632-687239,
 726408-728711, and 728096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

FEATURES source

1. .497
 /location/Qualifiers
 1. .497
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_idb="BT0616"
 /note="Organ: breast; Vector: pUC18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 2.69e-28 Length: 497
 Score: 290.00 Matches: 54
 Percent Similarity: 98.28% Conservative: 3
 Best Local Similarity: 93.10% Mismatches: 1
 Query Match: 94.46% Indels: 0
 DB: 2 Gaps: 0

US-10-031-158-14 (1-58) x AW087486 (1-497)

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuArgGlnSerSer 20
 Db 373 ATGGCAGATTTTCGCCAGCCACTATTTCTCCTGATGCTAACAACTCC 314

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgPheSerLeuMetLeuLeuArgTyr 40

Db	313	AGAACGCTGGACACACTTGTCTTCAGAAATTTCAGATATTAGATAC	BC017861
Qy	41	IleGlyLysSarGargAlaThrArgPheTrpAspProArgArgGlnThrPro 58	BC017861.1 GI:17389678
Db	253	ATTGCCAAGAAAGAGAGACACGATCTGGATCCAGGGACACCA 200	REFERENCE
			Authors
			Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z., and Han, Z.
			Organism
		Homo sapiens (human)	Mammalia; Buteraria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homidae; Homo.
			Keywords
			1 (bases 1 to 1510)
			COMMENT
			Unpublished (2000)
			Contact: Zeguang Han
			Chinese National Human Genome Center at Shanghai
			351 Guo Shoujing Road, ZhangJiang Hi-Tech Park, Pudong, Shanghai
			Tel: 86-21-50801922
			Fax: 86-21-50801945 (ex. 45)
			Email: hanzg@chgc.sh.cn
			This clone is available at CHGC in Shanghai.
			Location/Qualifiers
		1. . 681	1. . 1510
		/organism="Homo sapiens"	/organism="Homo sapiens"
		/mol_type="mRNA"	/mol_type="mRNA"
		/db_xref="taxon:9606"	/db_xref="IMAGE:4687960"
		/clone="DCBSCB09"	/tissue_type="Lung"
		/cell_type="dendritic cells"	/clone_Tax="NIH MGC_77"
		/dev_stage="mature"	/lab_host=DH10B"
		/lab_host="RN25.8"	note="Vector: pDNR-LIB"
		/clone_lib="DCB"	
		/notes="Vector: ptriplex2; Site_1: sfIIA; Site_2: sfIIB"	
			FEATURES
			source
			clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
			Series: IML Plate: 36 Row: k Column: 19
			This clone has the following problem: frame shifted.
			Location/Qualifiers
		1. . 1510	1. . 1510
		/organism="Homo sapiens"	/organism="Homo sapiens"
		/mol_type="mRNA"	/mol_type="mRNA"
		/db_xref="taxon:9606"	/db_xref="taxon:9606"
		/clone="IMAGE:4687960"	/clone="IMAGE:4687960"
		/tissue_type="Lung"	/tissue_type="Lung"
		/clone_Tax="NIH MGC_77"	/clone_Tax="NIH MGC_77"
		/lab_host=DH10B"	/lab_host=DH10B"
		note="Vector: pDNR-LIB"	note="Vector: pDNR-LIB"
			ORIGIN
			Alignment Scores:
			Pred. No.: 3.78e-28
			Score: 290.00
			Percent Similarity: 98.28%
			Best Local Similarity: 93.10%
			Query Match: 94.46%
			DB: 3
			Gaps: 0
			US-10-031-158-14 (1-58) x BC017861 (1-1510)
			Qy 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLysGlnSerSer 20
			Db 179 ATGCAGATGTTCCCTCCAGCCACTATTTCTCTCTGATGTTCTGAAACAACTCC 238
			21 ArgArgLeuGluHisThrPheValPheLeuArgLysPheSerLeuMetLeuLeuArgArg 40
			239 AGAGGCTGCGAACATACATCTTGTCCTCTGAGATTTCCAGATATTAGATAC 298
			41 IleGlyLysSarGargAlaThrArgPheTrpAspProArgArgGlnThrPro 58
			Db 299 ATGGCAGAGAGAGAGAGACACGATCTGGATCCAGGGACACCA 352
			RESULT 23
			BPF64904
			LOCUS BPF64904 1055 bp mRNA linear EST 22-JAN-2001
			DEFINITION B0262961 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4357102 5'
			ACCESSION BP96404
			VERSION BP96404.1 GI:12332119
			KEYWORDS EST.
			DEFINITION Homo sapiens. Similar to T cell receptor gamma locus, clone IMAGE:4687960, mRNA.
			RESULT 22
			BC017861
			LOCUS BC017861 1510 bp mRNA linear HTC 06-DEC-2001

SOURCE	Homo sapiens (human)	REFERENCE	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM		AUTHORS	1 (bases 1 to 523)
LOCUS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	TITLE	NIH-MGC http://mgc.nci.nih.gov/
DEFINITION	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
ACCESSION	1 (bases 1 to 1055)	COMMENT	Unpublished (1999)
VERSION	NIH-MGC	CONTACT	Robert Strauberg, Ph.D.
KEYWORDS		E-mail:	cgbps-r@mail.nih.gov
SOURCE		Tissue Procurement:	CLONETECH Laboratories, Inc.
ORGANISM	Homo sapiens (human)	CDNA Library Preparation:	CLONETECH Laboratories, Inc.
		CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNL)
		DNA Sequencing by:	Incyte Genomics, Inc.
		Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
PLATE:	LICM217 row: o column: 23	Plate:	LICM105 row: m column: 23
FEATURES	High quality sequence stop: 587.	FEATURES	High quality sequence stop: 510.
SOURCE	Location/Qualifiers	SOURCE	Location/Qualifiers
	1. 1055		1. .523
	/organism="Homo sapiens"		/organism="Homo sapiens"
	/mol_type="mRNA"		/mol_type="mRNA"
	/db_xref="taxon:9606"		/db_xref="taxon:9606"
	/lab_host="DH10B (T1 phage-resistant)"		/lab_host="DH10B (T1 phage-resistant)"
	/clone_lib="NIH_MGC_81"		/clone_lib="NIH_MGC_83"
	/note="Organ: muscle (skeletal); Vector: PDNR-LIB		/note="Organ: prostate; Vector: PDNR-LIB (Clontech);
	(Clontech); Site 1: SfiI (ggccgcctggcc); Site 2: SfiI (ggccattatggcc); 5', and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTAGGCC-3', and 3' adaptor sequence: 5'-ATTCAGGGCGGAGGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.5-4.0 kb). 1415 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."		Site 1: SfiI (ggccgcctggcc); Site 2: SfiI (ggccattatggcc); 5', and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTAGGCC-3', and 3' adaptor sequence: 5'-ATTCAGGGCGGAGGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 1415 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN		ORIGIN	
Alignment Scores:		Alignment Scores:	
Pred. No.:	8.658-28	Length:	523
Score:	289.00	Matches:	57
Percent Similarity:	98.31%	Conservative:	0
Best Local Similarity:	96.61%	Mismatches:	1
Query Match:	94.14%	Indels:	1
DB:	2	Gaps:	0
US-10-031-158-14 (1-58) x BF964904 (1-1055)		US-10-031-158-14 (1-58) x BF675605 (1-523)	
Qy	1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20	Qy	1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20
Db	67 ATGAGCATGTTCCCCAACGCCACTATTTCCTCTCAATTGCTGAACAAAGCTC 126	Db	64 ATGAGCATGTTCCCCAACGCCACTATTTCCTCTCAATTGCTGAACAAAGCTC 123
Qy	21 ArgArgGluGluIstThrPhe-ValPheLeuIargIasnPheSerLeuUmeLeuLeuArgY 40	Qy	21 ArgArgGluGluIstThrPhe-ValPheLeuIargIasnPheSerLeuUmeLeuLeuArgY 40
Db	127 AGAGGCTGGACATACCTTGCTCTGAGACATTTCCCTGTATGTTAAGATA 186	Db	124 AGAGGCTGGACATACCTTGCTCTGAGACATTTCCCTGTATGTTAAGATA 183
Qy	40 KileGlyIlysSarGargAlaThrArgPheTrpAspProArgArgGlyIlysThrPro 58	Qy	40 KileGlyIlysSarGargAlaThrArgPheTrpAspProArgArgGlyIlysThrPro 58
Db	187 CATGGGAGAGAGAGAGACACAGATTCTGGATCCAGAGAGAACACACCA 241	Db	184 CATGGGAGAGAGAGACACAGATTCTGGATCCAGAGGGAGAACACACCA 238
RESULT 24		RESULT 25	
BF675605	BF675605 523 bp mRNA linear EST 21-DEC-2000	LOCUS	A1758378/c
DEFINITION	602083495F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4247998 5', mRNA sequence.	DEFINITION	A1758378
ACCESSION	BF675605	DEFINITION	362 bp mRNA linear EST 07-MAR-2000
VERSION	BF675605.1 GI:11949500	DEFINITION	ty69c12.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:228446 3', similar to gb:W13231 T-CELL RECEPTOR GAMMA CHAIN C REGION (HUMAN), mRNA sequence.
KEYWORDS		ACCESSION	A1758378
SOURCE	Homo sapiens (human)	VERSION	A1758378.1 GI:5152101
ORGANISM	Homo sapiens	KEYWORDS	
		SOURCE	
		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 362)	REFERENCE	1 (bases 1 to 362)

AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbps-b@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmerich-Buck, M.D., Ph.D. Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution by: Washington University clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bbrp/image/image.html Insert Length: 774 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 286.
FEATURES	Location/Qualifiers
SOURCE	1. .362 <organism="Homo sapiens"> <mol_type="mRNA"> <db_xref="taxon:9606"> <clone>IMGR:2284246 <lab host="NH10B"> <clone lib="NCI-CGAP_kid11"> <note=Organ: kidney; Vector: pTR3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; plasmid DNA from the normalized library NCI-CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from a pool of 5,000 clones made from the same library (cloneIDs 132376-132911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. " subtraction by Bento Soares and M.
ORIGIN	Alignment Scores: Pred. No.: 1.13e-27 Length: 362 Score: 284.00 Matches: 53 Percent Similarity: 96.58% Conservative: 3 Best Local Similarity: 91.38% Mismatches: 2 Query Match: 92.51% Indels: 0 DB: Gaps: 0
US-10-031-158-14 (1-58) x AI758378 (1-362)	Alignment Scores: Pred. No.: 1.13e-27 Length: 362 Score: 284.00 Matches: 53 Percent Similarity: 96.58% Conservative: 3 Best Local Similarity: 91.38% Mismatches: 2 Query Match: 92.51% Indels: 0 DB: Gaps: 0
QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20	Alignment Scores: Pred. No.: 1.61e-26 Length: 719 Score: 278.00 Matches: 57 Percent Similarity: 98.28% Conservative: 0 Best Local Similarity: 98.28% Mismatches: 1 Query Match: 90.55% Indels: 1 DB: Gaps: 0
Db 349 ATGCAGATGTTCCGCCAGCCACTATTATCTTCCTGATGCTGAAACAACTCC 290	US-10-031-158-14 (1-58) x BR681238 (1-719)
QY 21 ArgArgLeuGluHisThrPheValPheLeuGlnGlnPheSerLeuLeuLeuArgTyr 40	Alignment Scores: Pred. No.: 1.61e-26 Length: 719 Score: 278.00 Matches: 57 Percent Similarity: 98.28% Conservative: 0 Best Local Similarity: 98.28% Mismatches: 1 Query Match: 90.55% Indels: 1 DB: Gaps: 0
Db 289 AGAAGCTGTCAACATACCTTGCTCTTGAGAATTTCCTCAGATATTAAGATAC 230	QY 21 ArgArgLeuGluHisThrPheValPheLeuGlnGlnPheSerLeuLeuLeuArgTyr 40
QY 41 IleGlyLysArgArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58	Db 68 ATGCAGATGTTCCGCCAGCCACTATTATCTTCCTGCAATGCTGAAACAACTCC 127
Db 229 ATGGCAAGAAGAAGAGGAGCACAGATCTGGATCCAGGGAGAACCCA 176	QY 21 ArgArgLeuGluHisThrPheValPheLeuGlnGlnPheSerLeuLeuLeuArgTyr 40
RESULT 26	Db 128 AGAAGCTGTCAACATACCTTGCTCTTGAGAATTTCCTCAGATATTAAGATAC 186
BF681238	QY 41 IleGlyLysArgArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58
LOCUS BR681238	Db 187 ATGGGAGAAGAAGAGGAGCACAGATCTGGATCCAGGGAGAACCCA 240
DEFINITION 719 bp m _r NA linear EST 21-DEC-2000	RESULT 27
ACCESSION BR681238	BR681029
VERSION BR681238.1	DEFINITION BR681029
KEYWORDS EST.	ACCESSION BR681029
KEYWORD SOURCE Homo sapiens (human)	VERSION BR681029.1
ORGANISM Homo sapiens (human)	KEYWORD EST.
REFERENCE 1 (bases 1 to 719)	SOURCE Homo sapiens (human)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.	ORGANISM Burkittota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 854)	REFERENCE 1 (bases 1 to 854)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.	REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
REFERENCE 1 (bases 1 to 854)	AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
COMMENT Unpublished (1999)	COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.	COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabsr@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LNCM1148 row: b column: 09

High quality sequence stop: 518.

FEATURES

Source

Location/Qualifiers

1. .854

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4295104"

/lab_host="DPR-LIB (T1 phage-resistant)"

/clone_lib="NIH_MGC_83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgttggcc); Site 2: SfiI

(ggccattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence: 3'-ATTCCTAGAGGCCGAGGGCGACATG-dN (3')BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.4

kb (range 0.5-4.0 kb). 14/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA)."

ORIGIN

Alignment Scores:

Pred. No.: 2.3e-25

Length: 854

Score: 270.00

Matches: 53

Percent Similarity: 93.22%

Conservative: 2

Best Local Similarity: 89.83%

Mismatches: 3

Indels: 1

Query Match: 2

Gaps: 0

DB: US-10-031-158-14 (1-58) x BF681029 (1-854)

Qy 1 MetGIMMetPheProProSerProIleuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20

Db 65 ATGACAGATGTCCCCAAAGCCCACTATTTCCTCTTCAATGCTGAAACAAGCTCC 124

Qy 21 ArgArgLeuGluIleIleThrPheValPheLeuArgAgnPhsSerIleMetIleLeuLeuArgTy 40

Db 125 AGAACGCTGGACACATACCTTGTCTCTTGAGAATTTCCCTGATGTTCAATGATRAGAT 184

Qy 40 IleGlyIlysIysBsrGargAlaIleThrArgPheTrpAspPproArgArgLysGlyIlyPro 58

Db 185 ACATGGCAAGAAAGAGAGAACACGATTCTGGATCCGGAGGGAAACACCA 239

RESULT 28

BF679165

LOCUS 602153737F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294761 5',

DEFINITION mRNA Sequence.

ACCESSION BFR79165

VERSION BFR79165.1 GI:11953060

KEYWORDS SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens (human)

REFERENCE

National Institutes of Health, Mammalian Gene Collection (MGC)

1 (bases 1 to 629)

NIM-MGC http://mgc.ncbi.nlm.nih.gov/.

Bimaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Unpublished (1999)

COMMENT Contact: Robert Straubberg, Ph.D.

Email: cgabsr@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

JOURNAL DNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Unpublished (1999)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LNCM1148 row: b column: 09

High quality sequence stop: 518.

Location/Qualifiers

1. .629

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4224761"

/clone_lib="NIH_MGC_83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgttggcc); Site 2: SfiI

(ggccattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence: 3'-ATTCCTAGAGGCCGAGGGCGACATG-dN (3')BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.4

kb (range 0.5-4.0 kb). 14/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA)."

ORIGIN

Alignment Scores:

Pred. No.: 2.96e-25

Length: 629

Score: 268.00

Matches: 55

Percent Similarity: 94.83%

Conservative: 0

Best Local Similarity: 94.83%

Mismatches: 3

Indels: 1

Query Match: 2

Gaps: 0

DB: US-10-031-158-14 (1-58) x BR679165 (1-629)

Qy 1 MetGIMMetPheProProSerProIleuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20

Db 67 ATGCAAGATGTCCCCAACGCCACTATTTCCTCTTCAATGCTGAAACAAGCTCC 126

Qy 21 ArgArgLeuGluIleIleThrPheValPheLeuArgAgnPhsSerIleMetIleLeuLeuArgTy 40

Db 127 AGAGGCTGGACACATACCTTGTCTCTTGAGAATTTCCCTGATGTTAGATA 185

Qy 41 IleGlyIlysIysBsrGargAlaIleThrArgPheTrpAspPproArgArgLysGlyIlyPro 58

Db 187 AT-GGCAAGAAAGAGAGAACACGATTCTGGATCCGGAGGGAGACACCA 239

RESULT 29

BF680840

LOCUS 602156088F1 NIH_MGC_83 Homo sapiens mRNA linear EST 21-DEC-2000

DEFINITION mRNA sequence.

ACCESSION BFR680840

VERSION BFR680840.1 GI:11954735

KEYWORDS SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

National Institutes of Health, Mammalian Gene Collection (MGC)

1 (bases 1 to 803)

NIM-MGC http://mgc.ncbi.nlm.nih.gov/.

Bimaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Unpublished (1999)

COMMENT Contact: Robert Straubberg, Ph.D.

Email: cgabsr@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

JOURNAL DNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Unpublished (1999)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LNCM1148 row: J column: 10

High quality sequence stop: 627.

Location/Qualifiers

1. .627

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4224761"

/clone_lib="NIH_MGC_83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgttggcc); Site 2: SfiI

(ggccattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence: 3'-ATTCCTAGAGGCCGAGGGCGACATG-dN (3')BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.4

kb (range 0.5-4.0 kb). 14/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA)."

ORIGIN

Alignment Scores:

Pred. No.: 2.96e-25

Length: 629

Score: 268.00

Matches: 55

Percent Similarity: 94.83%

Conservative: 0

Best Local Similarity: 94.83%

Mismatches: 3

Indels: 1

Query Match: 2

Gaps: 0

DB: US-10-031-158-14 (1-58) x BR679165 (1-629)

Qy 1 MetGIMMetPheProProSerProIleuPhePhePheLeuGlnLeuLeuIysGlnSerSer 20

Db 67 ATGCAAGATGTCCCCAACGCCACTATTTCCTCTTCAATGCTGAAACAAGCTCC 126

Qy 21 ArgArgLeuGluIleIleThrPheValPheLeuArgAgnPhsSerIleMetIleLeuLeuArgTy 40

Db 127 AGAGGCTGGACACATACCTTGTCTCTTGAGAATTTCCCTGATGTTAGATA 185

Qy 41 IleGlyIlysIysBsrGargAlaIleThrArgPheTrpAspPproArgArgLysGlyIlyPro 58

Db 187 AT-GGCAAGAAAGAGAGAACACGATTCTGGATCCGGAGGGAGACACCA 239

RESULT 29

BF680840

LOCUS 602156088F1 NIH_MGC_83 Homo sapiens mRNA linear EST 21-DEC-2000

DEFINITION mRNA sequence.

ACCESSION BFR680840

VERSION BFR680840.1 GI:11954735

KEYWORDS SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

National Institutes of Health, Mammalian Gene Collection (MGC)

1 (bases 1 to 803)

NIM-MGC http://mgc.ncbi.nlm.nih.gov/.

Bimaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Unpublished (1999)

COMMENT Contact: Robert Straubberg, Ph.D.

Email: cgabsr@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

JOURNAL DNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Unpublished (1999)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LNCM1148 row: J column: 10

High quality sequence stop: 627.

Location/Qualifiers

1. .627

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4224761"

/clone_lib="NIH_MGC_83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site 1: SfiI (ggccgttggcc); Site 2: SfiI

(ggccattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence: 3'-ATTCCTAGAGGCCGAGGGCGACATG-dN (3')BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.4

kb (range 0.5-4.0 kb). 14/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA)."

found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
 Plate: LNCM150 row: o column: 22
 High quality sequence stop: 689.
 Location/Qualifiers

FEATURES source

1. .803
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:606"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone.lib="NIH MGC 83"
 /note="Organ: prostate; Vector: PDR-LIB (Clontech);
 Site 1: SfiI (ggccgcctggcc); Site 2: SfiI
 (ggccatgtggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCATATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGGCGAGGCCGACATG-CG (3.0)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14115 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Alignment Scores:

Pred. No.:	5.389-25	Length:	803
Score:	267.00	Matches:	57
Percent Similarity:	96.61%	Conservative:	0
Best Local Similarity:	96.61%	Mismatches:	1
Query Match:	86.97%	Indels:	2
DB:		Gaps:	0

US-10-031-158-14 (1-58) x BF680840 (1-803)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGinSerSer 20
 67 ATGCGATGTTCGCCAAAGCCCACTATTTCCTCTCTCATG-CTGAAACAAAGCTCC 125

QY 21 ArgArgLeuLysThrPheValPheLeuGlnPheSerLeuLeuMetLeuLeuArgTr 40
 126 AGAAGGCTGCAACATACTTGTCTCTGGAATTTTCCCTGATGTTAGAAC 185

QY 41 IleGly-LysBlaArgGalaThrArgPheTrpAspProArgArgGlyThrPro 58
 186 ATAGCCAAAAGAAAAGAGACACAGATCTGGATCCAGGGGGAAACCCA 240

RESULT 30

BI836020 LOCUS B1836020 772 bp mRNA linear EST 04-OCT-2001
 DEFINITION 60308004F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223193 5',
 mRNA sequence.

ACCESSION BI836020
 VERSION BI836020.1 GI:15947570

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgs@nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
 Plate: LNCM1087 row: m column: 09
 High quality sequence stop: 522.
 Location/Qualifiers

1. .808
 /organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES source

High quality sequence stop: 768.
 Location/Qualifiers

1. .772
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /lab_host="DH10B"
 /clone.lib="NIH MGC 120"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb insert size range 1.2-5.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2.39e-24	Length:	772
Score:	262.00	Matches:	54
Percent Similarity:	93.33%	Conservative:	2
Best Local Similarity:	90.00%	Mismatches:	2
Query Match:	85.34%	Indels:	2
DB:		Gaps:	0

US-10-031-158-14 (1-58) x B1836020 (1-772)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGinSerSer 20
 427 ATGCGATGTTCGCCAAAGCCCACTATTTCCTCTCATG-CTGAAACAAAGCTCC 486

QY 21 ArgArgLeuLysThrPheValPheLeu-ArgAsnPheSerLeuLeuMetLeuLeuArgTr 40
 487 AGAAGGCTGCAACATACTTGTCTCTGGAATTTTCCCTGATGTTAGAAC 546

QY 40 IleGly-LysBlaArgGalaThrArgPheTrpAspProArgArgGlyThrPro 58
 547 CATGGCAAGCAAAGAGACACAGATCTGGATCCAGGAGGAACCCA 602

RESULT 31

BF673289 LOCUS BF673289 808 bp mRNA linear EST 21-DEC-2000
 DEFINITION 60213613F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272944 5',
 mRNA sequence.

ACCESSION BF673289
 VERSION BF673289.1 GI:11947184

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgs@nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
 Plate: LNCM1087 row: m column: 09
 High quality sequence stop: 522.
 Location/Qualifiers

1. .808
 /organism="Homo sapiens"

/db_xref="taxon:5606"
 /clone="IMAGE:27294"
 /lab_host="DHL0B (T1 phage-resistant)"
 /clone_lib="NIH MGC_83"
 /note="Organ: prostate; vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggccgcctcgcc); Site_2: SfiI
 (ggccattatgcc); 5', and 3', adaptors were used in cloning,
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3',
 and 3' adaptor sequence: 5'-CACGCCATTATGCC-3'
 Site_1: SfiI (ggccgcctcgcc); Site_2: SfiI
 (ggccattatgcc); 5', and 3', adaptors were used in cloning,
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3',
 and 3' adaptor sequence: 5'-CACGCCATTATGCC-3'
 C' or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN

Alignment Scores:
 Pred. No.: 6.33e-24 Length: 808
 Score: 259.00 Matches: 56
 Percent Similarity: 93.44% Conservative: 1
 Best Local Similarity: 91.80% Mismatches: 1
 Query Match: 84.36% Indels: 3
 DB: Gaps: 0

US-10-031-158-14 (1-58) x BF673289 (1-808)

Qy 1 MetGlnMetpheProProSerProleuPhephephepheLeuGln-LeuLeuLysGlnSerSer 20
 Db 286 ATGCAGATGTTCCTCCAAAGCCCACTATTTCCTCTCTCATGCTGAGAACAGCTC 345
 Qy 20 RArgArgLeuGluHiThrPhe-ValPheLeuArgAsnPheSerLeuMetLeuLeuArgT 40
 Db 346 CAGAAAGCTGGRACATACACTTGTTGTCCTCTGGAAATTTCCTGGATGTTATTAAGAT 405
 Qy 40 YIleGLYLYSlysGargGalaThrArgPheTrpAspProArgArgYIlePro 58
 Db 406 ACATTTGGCANGAAGAAGGCAACAGATCTGGATCCAGGAGGGACACCA 462

RESULT 32

BF674457 LOCUS BF674457 857 bp mRNA linear EST 21-DEC-2000
 DEFINITION 602137231F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273734 5',
 mRNA sequence.

ACCESSION BF674457
 VERSION BF674457.1 GT:11948352
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.ncbi.nih.gov/

REFERENCE 1 (bases 1 to 857)
 AUTHORS NIH-MGC
 TITLE NIH-MGC
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabre@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 DNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 DNA Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://Image.Lnl.gov
 Plate: LNCM143 row: n column: 07
 High quality sequence stop: 638.

FEATURES source
 Location/Qualifiers
 1. 857 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4294386"
 /lab_host="DHL0B (T1 phage-resistant)"
 /db_xref="taxon:9606"
 /clone="IMAGE:4273734"
 /lab_host="DHL0B (T1 phage-resistant)"
 /clone="IMAGE:4273734"
 /lab_host="DHL0B (T1 phage-resistant)"

ORIGIN

Alignment Scores:
 Pred. No.: 4.29e-23 Length: 857
 Score: 253.00 Matches: 56
 Percent Similarity: 96.55% Conservative: 0
 Best Local Similarity: 96.55% Mismatches: 2
 Query Match: 82.41% Indels: 2
 DB: Gaps: 0

US-10-031-158-14 (1-58) x BF674457 (1-857)

Qy 1 MetGlnMetpheProProSerProleuPhephephepheLeuGlnLeuLeuLysGlnSerSer 20
 Db 63 ATGCAGATGTTCCTCCAAAGCCCACTATTTCCTCTCATGCTGAGAACAGCTC 121
 Qy 21 ArgArgLeuGluHiThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyr 40
 Db 122 AGAAAGCTGGRACATACACTTGTTGTCCTCTGGAAATTTCCTGGATGTTATTAAGATC 181
 Qy 41 IleGLYLYSlysGargGalaThrArgPheTrpAspProArgArgYIlePro 58
 Db 182 AT-GGCAAGAAGAGAGACACGATCTGGATCCAGGAGGGACACCA 234

RESULT 33

BF679284 LOCUS BF679284 849 bp mRNA linear EST 21-DEC-2000
 DEFINITION 602153477F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294386 5',
 mRNA sequence.

ACCESSION BF679284
 VERSION BF679284.1 GI:11953179
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.ncbi.nih.gov/

REFERENCE NIH-MGC
 AUTHORS NIH-MGC
 TITLE NIH-MGC
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabre@mail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 DNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 DNA Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://Image.Lnl.gov
 Plate: LNCM143 row: j column: 19
 High quality sequence stop: 587.
 Location/Qualifiers

FEATURES source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4294386"
 /lab_host="DHL0B (T1 phage-resistant)"
 /db_xref="taxon:9606"
 /clone="IMAGE:4273734"
 /lab_host="DHL0B (T1 phage-resistant)"
 /clone="IMAGE:4273734"
 /lab_host="DHL0B (T1 phage-resistant)"

(clone Lib=NIH MGC_83)
 /note="Organ: prostate; vector: pDNR-LIB (Clontech),
 Site_1: SfiI (ggccgcctcgcc); Site_2: SfiI
 (ggccattatgcc); 5', and 3', adaptors were used in cloning,
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3',
 and 3' adaptor sequence: 5'-CACGCCATTATGCC-3'
 5'-ATTCTAGAGCCGGAGCGGACATG-AT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

(ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'; and 3' adaptor sequence: 5'-ATTCAGACCCGAGGCCGACATG-*dt*(30)BN-3' (where B = A, C', or G and N = A, C', G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 1415 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).

ORIGIN

Alignment Scores:

Pred. No.: 7.84e-23
Score: 251.00
Percent Similarity: 96.55%
Best Local Similarity: 96.55%
Query Match: 81.76%

Length: 849
Matches: 56
Conservative: 0
Mismatches: 2
Indels: 2
Gaps: 0

DB:

Query Match:

DB:

Alignment Scores:

Pred. NO.:	3.698-22	Length:	663
Score:	245.00	Matches:	48
Percent Similarity:	89.66%	Conservative:	4
Best Local Similarity:	82.76%	Mismatches:	6
Query Match:	79.80%	Indels:	0
DB:	6	Gaps:	0

US-10-031-158-14 (1-58) x CB553506 (1-663)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnIleLeuIysGlnSerSer 20
Db 401 ATGCAGATGTTCACTTCAAGCCACTATATTCTTCCTTCATGCTGAAACAAACCTCC 460
QY 21 ArgArgLeuGluHisThrPheLeuValPheLeuArgAlaPhsSerLeuMetLeuLeuArgTyr 40
Db 461 ACAAGGCTGGACATACCTTGCTCTGAGAATTTCGCCAGAGGGAAACCCA 520
QY 41 IleGlyLysLySarGargAlaThrArgPheTerpApproArgArgGlyThrPro 58
Db 521 ATTGGCAAGAAAGACAGCACAAAGGTCTCGAAATCCCAAGAGGGAAACCCA 574

RESULT 36

BF678129	BR678129	870 bp mRNA linear EST 21-DEC-2000
DEFINITION	60208581F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249245 5', mRNA sequence.	
ACCESSION	BR678129	
VERSION	BR678129.1 GI:11952024	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 870)	
AUTHORS	Eikarova; Metzger; Chordata; Craniata; Vertebrates; Euteleostomi; mRNA sequence.	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbsr@mail.nih.gov Title: Procurement: CLONETECH Laboratories, Inc. CDNA library Preparation: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: LUCM69 row: a column: 22 High quality sequence stop: 557.	

FEATURES

source	Location/Qualifiers
1. 870	/organism="Homo sapiens"
/mol_type="mRNA"	/db_xref="taxon:9606"
/lab_host="DHIOB (T1 phage-resistant)"	/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: PPNR-LIB (Clontech); Site_1: SfI (ggccgcgtggc); Site_2: SfI (ggccatttcggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3', and 3' adaptor sequence: 5'-ATCTCAGAGGCCGAGGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."	
ORIGIN	

RESULTS

CB551454	CB551454	637 bp mRNA linear EST 01-JUN-2003
DEFINITION	MMSP0013_E12 MMSP Macaca mulatta cDNA, mRNA sequence.	
ACCESSION	CB551454	
VERSION	CB551454.1 GI:3130649	
KEYWORDS	EST.	
SOURCE	Macaca mulatta (rhesus monkey)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Butcheria; Primates; Catarhini; Cercopithecidae; Cercopithecinae; Macaca.	
REFERENCE	1 (baseee 1 to 637)	
AUTHORS	Katz, M.G., Bungarner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.	
TITLE	Expressed sequence tags from Rhesus macaque spleen	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Holzman, T Katz Lab University of Washington Box 358070, Seattle, WA 98195-8070, USA Tel: 206 732 6156 Fax: 206 732 6055 Email: ted@locke.ws.washington.edu Similar to GenBank entry S60779 S60779 Homo sapiens nonfunctional T-cell receptor gamma chain variable region mRNA, partial sequence. 8/2000	
PLATE	MMSP0013 row: E column: 12.	

FEATURES

source	Location/Qualifiers
1. .637	/organism="Macaca mulatta"
/mol_type="mRNA"	/db_xref="taxon:9544"
/sex="male"	/cell_type="monocyte"
/dev_stage="adult"	/clone_lib="MMSP"
/note="Organ: spleen"	

RESULTS

US-10-031-158-14 (1-58) x CB551454 (1-637)	Score: 227.00	Matches: 56
QY	Percent Similarity: 93.33%	Conservative: 0
Db	Best Local Similarity: 93.33%	Mismatches: 2
Query Match:	73.94%	Indels: 4
DB:	2	Gaps: 0

US-10-031-158-14 (1-58) x CB551454 (1-637)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnIleLeuIysGlnSerSer 20
Db 454 ATGCAGATGTTCACTTCAAGCCACTATTTCTCTTCATGCTGAAACATACTCC 513

ALIGNMENT SCORES:

Pred. NO.:	1.28e-19	Length:	637
Score:	226.00	Matches:	48
Percent Similarity:	86.44%	Conservative:	3
Best Local Similarity:	81.36%	Mismatches:	7
Query Match:	73.62%	Indels:	1
DB:	6	Gaps:	0

ORIGIN

Alignment Scores:

Pred. NO.:	1.28e-19	Length:	870
------------	----------	---------	-----

QY 21 ArgArgLeuGluIleIthrPheValPheLeuIleSerLeuLeuMetLeuLeuArgTyr 40
 514 ATAGGCTGGAACATACATCTTGTCTCTGAGAATTTCAGATGTTGAGATAC 573
 41 -IleGlyLysLysSarGalaThrArgPheTraspProArgArgGlyThrPro 58
 574 CATGCCAGAAAAGAACGAAACAGCAACAGGTCTGAATCCAGAGGGAAACCCA 628

RESULT 38
 DEFINITION BB677916 mRNA sequence.
 ACCESSION BG677916 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248993 5',
 VERSION BG677916.1 GI:11951811
 KEYWORDS EST.
 SOURCE JOURNAL
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 670)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: CLONTECH Laboratories, Inc.
 DNA Library Preparation: CLONTECH Laboratories, Inc.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Email: cgbps@mail.nih.gov
 Contact: Robert Strausberg, Ph.D.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium (ILNL) at:
<http://image.llnl.gov>
 Plate: LICM068 row: 9 column: 10
 High quality sequence stop: 668.

FEATURES source
 1. .670
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="mRNA"
 /clone="IMAGE:4248993"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 83"
 /note="organism: Homo sapiens"
 site_1: SfiI (ggccgcctcgcc); Site_2: SfiI (ggccatccggcc);
 (ggccattatggcc); 5' and 3' adaptors were used in cloning,
 as follows: 5' adaptor sequence: 5'-CAGGCCATATGGCC-3'
 and 3' adaptor sequence: 5'-ATCTAGAGCCGAGGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA)."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.37e-19 Length: 670
 Score: 224.00 Matches: 55
 Percent Similarity: 94.83% Conservative: 0
 Best Local Similarity: 94.83% Mismatches: 3
 Query Match: 72.96% Indels: 3
 DB: 2 Gaps: 0

US-10-031-158-14 (1-58) x BB677916 (1-670)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
 65 ATGCAAGATGTTCCCCAACGCCACTATTTCTCTCTCATG-CTGAAACAGCTCC 123
 21 ArgArgLeuGluIleIthrPheValPheLeuIleSerLeuLeuMetLeuLeuArgTyr 40

RESULT 39
 DEFINITION BG535408 mRNA sequence.
 ACCESSION BG535408 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4687960 5',
 VERSION BG535408 mRNA sequence.
 KEYWORDS EST.
 SOURCE JOURNAL
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 827)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: CLONTECH Laboratories, Inc.
 DNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: LICM1501 row: i column: 17
 High quality sequence stop: 609.
 Location/Qualifiers
 1. .827
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="Taxon:9606"
 /clone="IMAGE:687960"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="organ: lung; vector: pDR-LIB (Clontech); Site 1:
 SfiI (ggccgcctcgcc); Site 2: SfiI (ggccatccggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCCATATGGCC-3' and 3' adaptor sequence:
 5'-ATCTAGAGCCGAGGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."

ORIGIN
 Alignment Scores:
 Pred. No.: 7.64e-19 Length: 827
 Score: 221.00 Matches: 50
 Percent Similarity: 88.71% Conservative: 5
 Best Local Similarity: 80.65% Mismatches: 3
 Query Match: 71.99% Indels: 4
 DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x BG535408 (1-827)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLeuGlnSerSer 20
 489 ATCGAGATGTTCCCCAACGCCACTATTTCTCTCTCATG-CTGAAACAGCTCC 548
 549 AGAGGCTGAGAATCACCTTGTCTCTGAGAATGATCCAGATATAAGCAT 608
 QY 40 YrileGlyLysLysSarGalaThrArgPheTraspProArgArgGlyThrPro 58

RESULT 40

BR370026 BF370026 572 bp mRNA linear EST 24-NOV-2000
 LOCUS MR3-FN0004-120600-001-g12 FN0004 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BP370026 ACATGGGCACAGGAAACAGCAGCAACGGATTCTGGATTCAGGAGGGAAACCCCA 666
 ACCESSION BP370026.1 GI:11331960
 VERSION EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butherida; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1. (bases 1 to 572)
 AUTHORS Dias Neto, L., Garcia Correa, R., Verjovski-Almeida, S., Briunes, M.R.,
 Nagai, M.A., da Silva, W., Jr., Zago, M.A., Bordim, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H.,
 Brusstein, A., Doliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil.
 Tel: +55-11-2707001
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL:
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR3&t2=FN0004-120600-001-g12&t3=2000-06-12&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 19
 High quality sequence stop: 46.
 Location/Qualifiers
FEATURES
 source
 ORIGIN
 Alignment Scores:

Pred. No.:	1.97e-17	Length:	572
Score:	209.00	Matches:	44
Percent Similarity:	80.00%	Conservative:	4
Best Local Similarity:	73.33%	Mismatches:	10
Query Match:	68.08%	Indels:	2
DB:	2	Gaps:	0

 US-10-031-158-14 (1-58) x BF370026 (1-572)

QY 1 MetGlnMetPheProProSerProIlePhePhePheLeuGlnIleLeuIleGlnSerSer 20
 QY |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 21
 Db 7 ATGCAGATGATGCCAAGCCACTATATACTTCTCTGCTGAGAACAGCTC 66
 21 ArgArgGluGluLysThrPheValPheLeu--ArgAsnPheSerIleMetLeuLeuIleGlnArgT 40
 67 AGAGGCGCTGGACATACCTTGCCCTCTGAGAATTTTCCTGATGTATTAAGAT 126

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 8, 2004, 07:51:31 ; Search time 56 Seconds
(without alignments)
736.174 Million cell updates/sec

Title: US-10-031-158-14

Perfect score: 307

Sequence: 1 MQMPPPSPLFFLQLKQSS.....RYIGKKRATREWDPRQRGTP 58

Scoring table: BLOSUM62

Xgapext 10.0 , Xgapext 0.5
Ygapext 10.0 , Ygapext 0.5
Fgapext 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
-MODBL=f,frame+p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US-031158/runat_06122004_082700_15922/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFM=factap -SUFIX=rni -MINMATCH=0.1 -LOCPL=0
-LOCPXT=0 -UNITS=512 -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human&0.cda
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODEL=LOCAL -OUTFMT=sto -NORM=ext -HEAPSIZE=500 -MLNLEN=0 -MAXLEN=2000000000
-USER-US1031158 @CGN_1_1_54 @runat_06122004_082700_15922 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPROP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Issued_Patents_NA:*

```
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	RESULT 1	ALIGNMENTS
US-09-513-999C-679	; Sequence 679, Application US/09513999C	
	; Patent No. 6783961	
	; GENERAL INFORMATION:	
	; APPLICANT: Dumas Milne Edwards, J.B.	
	; ATTORNEY: Ductier, A.	
	; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.	
	; FILE REFERENCE: 59-US2-REG	
	; CURRENT APPLICATION NUMBER: US/09/513, 999C	
	; CURRENT FILING DATE: 2000-02-24	
	; PRIOR APPLICATION NUMBER: US 60/122, 487	
	; PRIOR FILING DATE: 1999-02-26	
	; NUMBER OF SEQ ID NOS: 36681	
	; SOFTWARE: Patent.PM	
	; SEQ ID NO: 679	
	; LENGTH: 426	
	; NAME/KEY: CDS	
	; LOCATION: 267..425	
	; ALIGNMENT SCORES:	
	Pred. No.: 1.64e-36	
	Score: 307.00	
	Percent Similarity: 100.00%	
	Best Local Similarity: 100.00%	
	Query Match: 100.00%	
	Gaps: 0	

	RESULT 1	ALIGNMENTS
US-09-513-999C-679	; Sequence 679, Application US/09513999C	
	; Patent No. 6783961	
	; GENERAL INFORMATION:	
	; APPLICANT: Dumas Milne Edwards, J.B.	
	; ATTORNEY: Ductier, A.	
	; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.	
	; FILE REFERENCE: 59-US2-REG	
	; CURRENT APPLICATION NUMBER: US/09/513, 999C	
	; CURRENT FILING DATE: 2000-02-24	
	; PRIOR APPLICATION NUMBER: US 60/122, 487	
	; PRIOR FILING DATE: 1999-02-26	
	; NUMBER OF SEQ ID NOS: 36681	
	; SOFTWARE: Patent.PM	
	; SEQ ID NO: 679	
	; LENGTH: 426	
	; NAME/KEY: CDS	
	; LOCATION: 267..425	
	; ALIGNMENT SCORES:	
	Pred. No.: 1.64e-36	
	Score: 307.00	
	Length: 426	
	Matches: 58	
	Conservative: 0	
	Mismatches: 0	
	Indels: 0	

	RESULT 1	ALIGNMENTS
US-09-513-999C-679	; Sequence 679, Application US/09513999C	
	; Patent No. 6783961	
	; GENERAL INFORMATION:	
	; APPLICANT: Dumas Milne Edwards, J.B.	
	; ATTORNEY: Ductier, A.	
	; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.	
	; FILE REFERENCE: 59-US2-REG	
	; CURRENT APPLICATION NUMBER: US/09/513, 999C	
	; CURRENT FILING DATE: 2000-02-24	
	; PRIOR APPLICATION NUMBER: US 60/122, 487	
	; PRIOR FILING DATE: 1999-02-26	
	; NUMBER OF SEQ ID NOS: 36681	
	; SOFTWARE: Patent.PM	
	; SEQ ID NO: 679	
	; LENGTH: 426	
	; NAME/KEY: CDS	
	; LOCATION: 267..425	
	; ALIGNMENT SCORES:	
	Pred. No.: 1.64e-36	
	Score: 307.00	
	Length: 426	
	Matches: 58	
	Conservative: 0	
	Mismatches: 0	
	Indels: 0	

	RESULT 1	ALIGNMENTS
US-09-513-999C-679	; Sequence 679, Application US/09513999C	
	; Patent No. 6783961	
	; GENERAL INFORMATION:	
	; APPLICANT: Dumas Milne Edwards, J.B.	
	; ATTORNEY: Ductier, A.	
	; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.	
	; FILE REFERENCE: 59-US2-REG	
	; CURRENT APPLICATION NUMBER: US/09/513, 999C	
	; CURRENT FILING DATE: 2000-02-24	
	; PRIOR APPLICATION NUMBER: US 60/122, 487	
	; PRIOR FILING DATE: 1999-02-26	
	; NUMBER OF SEQ ID NOS: 36681	
	; SOFTWARE: Patent.PM	
	; SEQ ID NO: 679	
	; LENGTH: 426	
	; NAME/KEY: CDS	
	; LOCATION: 267..425	
	; ALIGNMENT SCORES:	
	Pred. No.: 1.64e-36	
	Score: 307.00	
	Length: 426	
	Matches: 58	
	Conservative: 0	
	Mismatches: 0	
	Indels: 0	

QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLygInsSer 20
Db 94 ATGCAGATGTTCCCCAACCCACTATTTCCTCAATTGCGAAACAACTCC 153
QY 21 ArgArgIleGluHistPheValPheLeuArgAsnDheSerLeuMetLeuLeuArgTyr 40
Db 154 AGAGGCCGAGACATACTTGCTGCTGAGAATTTCCTGATGTTAAAGATAC 213
QY 41 IleGlyLysLysSarGalaThrArgPheThrPaspProArgArgGlyThrPro 58
Db 214 ATTGGCAGAAGAAGAGCACAGCATCTGGATCCAGGAGGGAAACCCA 267
RESULT 2
US-08-256-964A-18
; Sequence 18, Application US/08256964A
; Patent No. 5723309
; GENERAL INFORMATION:
; APPLICANT: BONNIEVILLE, Marc
; TITLE OF INVENTION: PRODUCTION OF SUBUNITS OF SOLUBLE T
; TITLE OF INVENTION: RECEPTORS BY CO-TRANSFECTION, USES OF THE PRODUCTS THUS
; TITLE OF INVENTION: OBTAINED
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Young & Thompson
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256 964A
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 92 14203
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: Reg. No. 5723309 32,925
; REFERENCE/DOCKET NUMBER: BE 94/449
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/521-2297
; TELEFAX: 703/885-0573
; TELEX: 249425
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 825 base pairs
; TYPE: nucleic acid
; STRANDBNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE: CDS
; LOCATION: 1..825
; DOCUMENT INFORMATION:
; DOCUMENT NUMBER: WO 94/12648
; FILING DATE: 25-NOV-1993
; PUBLICATION DATE: 09-JUN-1994
; US-08-256-964A-18
; Alignment Scores:
; Pred. No.: 8.9e-32 Length: 1080
; Score: 279.00 Matches: 53
; Percent Similarity: 96.55% Conservatives: 3
; Best Local Similarity: 91.38% Mismatches: 2
; Query Match: 90.88% Indels: 0
; DB: 6 Gaps: 0
; US-10-031-158-14 (1-58) x 5260223-3 (1-1080)
; QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLygInsSer 20
; Db 452 ATGCAGATGTTCCCCAACCCACTATTTCCTCAATTGCGAAACAACTCC 511
; QY 21 ArgArgIleGluHistPheValPheLeuArgAsnDheSerLeuMetLeuLeuArgTyr 40
; Db 512 AGAGGCCGAGACATACTTGCTGCTGAGAATTTCCTGATGTTAAAGATAC 571
; QY 41 IleGlyLysLysSarGalaThrArgPheThrPaspProArgArgGlyThrPro 58
; Db 572 ATTGGCAGAAGAAGAGCACAGCATCTGGATCCAGGAGGGAAACCCA 625
; RESULT 4
; US-09-13-999C-8197
; Sequence 8197, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duleckt, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2. REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26

US-10-031-158-14 (1-58) x US-08-256-964A-18 (1-825)
QY 1 MetGlnMetPheProProSerProLeuPhePheLeuGlnLeuLeuLygInsSer 20
Db 440 ATGCAGATGTTCCCCAACCCACTATTTCCTCAATTGCGAAACAACTCC 499
QY 21 ArgArgIleGluHistPheValPheLeuArgAsnDheSerLeuMetLeuLeuArgTyr 40
Db 500 AGAGGCCGAGACATACTTGCTGCTGAGAATTTCCTGATGTTAAAGATAC 559
QY 41 IleGlyLysLysSarGalaThrArgPheThrPaspProArgArgGlyThrPro 58
Db 560 ATTGGCAGAAGAAGAGCACACGATTCTGGATCCAGGAGGGAAACCCA 613

RESULT 3
5260223-3
; Patent No. 5260223
; APPLICANT: BRENNER, MICHAEL B.; STROMINGER, JACK L.; SEIDMAN, JOHN G.; IP, STEPHEN H.; KRAMEL, MICHAEL S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF HUMAN GAMMA
; T CELL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/187, 638
; FILING DATE: 29-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 115, 256
; FILING DATE: 29-OCT-1987
; APPLICATION NUMBER: 16, 252
; FILING DATE: 19-FEB-1987
; APPLICATION NUMBER: 882, 100
; FILING DATE: 03-JUL-1986
; SEQ ID NO: 3
; LENGTH: 1080
; 5260223-3

Alignment Scores:
Pred. No.: 8.9e-32 Length: 1080
Score: 279.00 Matches: 53
Percent Similarity: 96.55% Conservatives: 3
Best Local Similarity: 91.38% Mismatches: 2
Query Match: 90.88% Indels: 0
DB: 6 Gaps: 0

NUMBER OF SEQ ID NOS: 36681
 SOFTWARE: Patent.pm
 SEQ ID NO: 8197
 LENGTH: 460
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: LOCATION: 327
 FEATURE: NAME/KEY: misc_feature
 LOCATION: 421
 OTHER INFORMATION: LOCATION: 422
 FEATURE: NAME/KEY: misc_feature
 OTHER INFORMATION: LOCATION: n=a, g, c or t
 S-09-513-999C-8197

ALIGNMENT SCORES:
 Pred. No.: 9.03
 Score: 65.50
 Percent Similarity: 63.04%
 Best Local Similarity: 39.93%
 Query Match: 21.34%
 DB: 4
 Gaps: 1

US-10-031-158-14 (1-58) x US-09-142-108C-1 (1-1789)
 Qy 4 PheProProserProleuPhePheLeuGlnLeuLeuLysGlnSerSerArgArgIleu
 Db 912 TTCCCTTCATATT-ATCCGCATCATCATTTAGAGAGATCAGTACACACATC 854
 Qy 24 GluHisThrRhevalPheLeuArgLysPheSerIleuMetIleuLeuArgTrileGlylys 43
 Db 853 TTTCAT-----TTCTCCAATAATTACCTTATGCTCTCAAGTATATCAGTCAA 803
 Qy 44 LysArgGargAlaThrArg 49
 Db 802 GAACGGCTCGAACCGGC 785

RESULT 6
 US-09-250-609-85
 ; Sequence 85, Application US/09250609A
 ; Patent No. 6458943
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrne, Jennifer A.
 ; TITLE OF INVENTION: Members of the D52 Gene Family
 ; FILE REFERENCE: 1383.0210002
 ; CURRENT APPLICATION NUMBER: US/09/250,609A
 ; CURRENT FILING DATE: 1999-02-17
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 85
 ; LENGTH: 503
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-250-609-85

ALIGNMENT SCORES:
 Pred. No.: 2.5
 Score: 64.00
 Percent Similarity: 59.25%
 Best Local Similarity: 48.15%
 Query Match: 20.85%
 DB: 4
 Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-609-85 (1-503)
 Qy 31 ArgAsnPheSerLeuMetIleuLeuArgArgTyrlIleGlyLysBargArgAlaThraPhe 50
 Db 246 AGGAGCTTCGGCTTGAGCTCTAAGGTGGAAAGAATGTCACTCTGGCAGGGTC 305
 Qy 51 TrpAspProArgArgGlyIle 57
 Db 306 TGGCAGCCANAGAGGACAT 326

RESULT 7
 US-09-250-611-85
 ; Sequence 85, Application US/09250611
 ; Patent No. 6528283
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrne, Jennifer A.
 ; APPLICANT: Basset, Paul
 ; TITLE OF INVENTION: Members of the D52 Gene Family
 ; FILE REFERENCE: 1383.0210001
 ; CURRENT APPLICATION NUMBER: US/09/250,611
 ; CURRENT FILING DATE: 1999-02-17
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 85
 ; LENGTH: 503

US-09-250-611-85 ; ORGANISM: Homo sapiens
 Alignment Scores: ;
 Pred. No.: 2.5 ; Length: 503 ;
 Score: 64.00 ; Matches: 13 ;
 Percent Similarity: 59.26% ; Conservative: 3 ;
 Best Local Similarity: 48.15% ; Mismatches: 11 ;
 Query Match: 20.85% ; Indels: 0 ;
 DB: 4 ; Gaps: 0 ;
 US-10-031-158-14 (1-58) x US-09-250-611-85 (1-503)
 Qy 31 ArgAsnPheSerIleMetLeuLeuArgTyrIleGlyLysArgGalaThrArgPhe 50
 Db 246 AGGAGCTTCGGGTAGGCTTGCTTAAAGGAAGAATTCACCTGCCCCAGGTGC 305
 Qy 51 TTPAProArgArgGlyThr 57
 Db 306 TGGCAGCCAAAGAGAGGACT 326
 RESULT 8 ;
 US-09-685-853A-3 ;
 Sequence 3 ; Application US/09685853A ;
 Patent No. 6479270 ;
 GENERAL INFORMATION: ;
 APPLICANT: WEI Ming-Hui et al. ;
 TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS, NUCLEAR ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS, TITLE OF INVENTION: AND USES THEREOF ;
 FILE REFERENCE: CLO00871 ;
 CURRENT APPLICATION NUMBER: US/09/685, 853A ;
 PRIORITY FILING DATE: 2002-05-06 ;
 PRIORITY APPLICATION NUMBER: 60/182, 194 ;
 PRIOR FILING DATE: 2000-02-14 ;
 NUMBER OF SEQ ID NOS: 3 ;
 SOFTWARE: FastSEQ for Windows Version 4.0 ;
 SEQ ID NO 3 ;
 LENGTH: 74962 ;
 TYPE: DNA ;
 ORGANISM: Homo sapien ;
 FEATURE: NAME/KEY: misc_feature ;
 LOCATION: (1..(74962)) ;
 OTHER INFORMATION: n = A,T,C or G ;
 US-09-685-853A-3
 Alignment Scores: ;
 Pred. No.: 3.55e+03 ; Length: 74962 ;
 Score: 63.50 ; Matches: 22 ;
 Percent Similarity: 47.62% ; Conservative: 8 ;
 Best Local Similarity: 34.92% ; Mismatches: 15 ;
 Query Match: 20.68% ; Indels: 18 ;
 DB: 4 ; Gaps: 3 ;
 US-10-031-158-14 (1-58) x US-09-685-853A-3 (1-74962)
 Qy 10 PhePhePheLeuGlnLeuLeuLysGlnSerSerArg-----Arg 22
 Db 44953 TTGTTTTTTCCTTCAAGTCACAGTGAATGTTGACTCTGTGTC 45012
 Qy 23 LeuGluHisThrPhe-VaPheLeuArgGlnPheSer-----Le 35
 Db 45013 ATAGAACCATACCTTCGTTTATGACTTGTGCTCTAGACTTGTGACTCTGTGAA 45072
 Qy 35 UMeLLLeuLeuArgTyrIleGlyLysArgGala-----ThrArgPheTpaS 52
 Db 45073 TGTCTCTGTAGGTTCATGAGCAGAGCACTTAGAGAACATCTTCTGTC 45132
 Qy 52 pProLrg 54
 Db 45133 TTAGAGA 45139
 RESULT 9 ;
 US-09-248-796A-10951 ;
 Sequence 10951 ; Application US/09248796A ;
 Patent No. 6747137 ;
 GENERAL INFORMATION: ;
 APPLICANT: Keith Weinstock et al. ;
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN FOR DIAGNOSTICS AND THERAPEUTICS ;
 FILE REFERENCE: 107196-132 ;
 CURRENT APPLICATION NUMBER: US/09/248, 796A ;
 CURRENT FILING DATE: 1999-02-12 ;
 PRIOR APPLICATION NUMBER: US 60/074, 725 ;
 PRIOR FILING DATE: 1998-02-13 ;
 PRIOR APPLICATION NUMBER: US 60/096, 409 ;
 PRIORITY FILING DATE: 1998-08-13 ;
 NUMBER OF SEQ ID NOS: 28208 ;
 SEQ ID NO 10951 ;
 LENGTH: 195 ;
 TYPE: DNA ;
 ORGANISM: Candida albicans ;
 US-09-248-796A-10951
 Alignment Scores: ;
 Pred. No.: 0.92 ; Length: 195 ;
 Score: 63.00 ; Matches: 10 ;
 Percent Similarity: 92.86% ; Conservative: 3 ;
 Best Local Similarity: 71.43% ; Mismatches: 1 ;
 Query Match: 20.52% ; Indels: 0 ;
 DB: 4 ; Gaps: 0 ;
 US-10-031-158-14 (1-58) x US-09-248-796A-10951 (1-195)
 Qy 3 MetPheProProSerProLeuPhePhePheLeuGlnLeuLeu 16
 Db 131 TATTCCTCCACCCCTTTTTTTTTTATCACTTAA 172
 RESULT 10 ;
 US-09-248-796A-11408 ;
 Sequence 11408 ; Application US/09248796A ;
 Patent No. 6747137 ;
 GENERAL INFORMATION: ;
 APPLICANT: Keith Weinstock et al. ;
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN FOR DIAGNOSTICS AND THERAPEUTICS ;
 FILE REFERENCE: 107196-132 ;
 CURRENT APPLICATION NUMBER: US/09/248, 796A ;
 CURRENT FILING DATE: 1999-02-12 ;
 PRIOR APPLICATION NUMBER: US 60/074, 725 ;
 PRIOR FILING DATE: 1998-02-13 ;
 PRIOR APPLICATION NUMBER: US 60/096, 409 ;
 PRIORITY FILING DATE: 1998-08-13 ;
 NUMBER OF SEQ ID NOS: 28208 ;
 SEQ ID NO 11408 ;
 LENGTH: 234 ;
 TYPE: DNA ;
 ORGANISM: Candida albicans ;
 US-09-248-796A-11408
 Alignment Scores: ;
 Pred. No.: 1.41 ; Length: 234 ;
 Score: 62.50 ; Matches: 17 ;
 Percent Similarity: 56.82% ; Conservative: 8 ;
 Best Local Similarity: 38.64% ; Mismatches: 18 ;
 Query Match: 20.36% ; Indels: 1 ;
 DB: 4 ; Gaps: 1 ;
 US-10-031-158-14 (1-58) x US-09-248-796A-11408 (1-234)
 Qy 9 LeuPhePhePheLeuGlnLeuLeuLysGlnSerSerArgArgLeuGluHisThr--Phe 27
 Db 31 TTAATTAACATTCTATTTCTATTAAGAAAAGAGGAAATTAGAGAACTCAATT 90
 Qy 28 ValPheLeuArgGlnPheSerIleMetLeuLeuArgTyrIleGlyLysArgGala 47

Db 91 TTTTTTTTGTGATTTCATCTTCTTCTTGTATTAGAAAAAAACCAT A 150 US-09-511-477-1
 Qy 48 ThRArgPheTrP 51
 Db 151 CCAAGATTTT 162

RESULT 11
 US-03-02-812-1
 ; Sequence 1, Application US/09302812B
 ; GENERAL INFORMATION:
 ; APPLICANT: JACOBSON, Myron K.
 ; APPLICANT: AM, Jean-Christophe
 ; APPLICANT: LIN, Winston
 ; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
 ; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
 ; FILE REFERENCE: NIAD 201
 ; CURRENT APPLICATION NUMBER: US/09/302,812B
 ; EARLIER FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 38
 ; SEQ ID NO 1
 LENGTH: 4070
 TYPE: DNA
 ORGANISM: Bos taurus
 FEATURE: ;
 Alignment Scores:
 pred. No.: 80.7 length: 4070
 Score: 62.50 Matches: 17
 Percent Similarity: 53.85% Conservative: 4
 Best Local Similarity: 43.59% Mismatches: 17
 Query Match: 20.36% Indels: 1
 DB: 3 3 Gaps: 1

US-09-302-812-1

Db 3293 ATGCAGTCCCTCCGCCATCGCAGTCAGTCTGACTCTGGCCCTCTCCATCCCCACTTA 3352

Qy 21 ArgArgLeuGluHisThr--PheValPheLeuArgAsnPheSerLeuMetLeuLeu
 DB: 3353 CATAGACTGAGACATACITGTTCTTCTTCTTCTTCAAGCCCTGATCTTIA 3409

RESULT 13
 US-09-511-507-1
 ; Sequence 1, Application US/09511507
 ; GENERAL INFORMATION:
 ; Patent No. 6395543
 ; APPLICANT: JACOBSON, Myron K.
 ; APPLICANT: AME, Jean-Christophe
 ; APPLICANT: LIN, Winston
 ; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
 ; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
 ; FILE REFERENCE: NIAD 201
 ; CURRENT APPLICATION NUMBER: US/09/511,507
 ; CURRENT FILING DATE: 2000-02-23
 ; PRIORITY FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 38
 ; SEQ ID NO 1
 LENGTH: 4070
 TYPE: DNA
 ORGANISM: Bos taurus
 FEATURE: ;
 US-09-511-507-1

Db 3293 ATGCAGTCCCTCCGCCATCGCAGTCAGTCTGACTCTGGCCCTCTCCATCCCCACTTA 3352

Qy 21 ArgArgLeuGluHisThr--PheValPheLeuArgAsnPheSerLeuMetLeuLeu
 DB: 3353 CATAGACTGAGACATACITGTTCTTCTTCTTCTTCAAGCCCTGATCTTIA 3409

RESULT 12
 US-09-511-477-1
 ; Sequence 1, Application US/09511477
 ; Parent No. 6317202
 ; GENERAL INFORMATION:
 ; APPLICANT: JACOBSON, Myron K.
 ; APPLICANT: AME, Jean-Christophe
 ; APPLICANT: LIN, Winston
 ; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
 ; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
 ; FILE REFERENCE: NIAD 201
 ; CURRENT APPLICATION NUMBER: US/09/511,477
 ; CURRENT FILING DATE: 2000-02-23
 ; PRIORITY FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 38
 ; SEQ ID NO 1
 LENGTH: 4070
 TYPE: DNA
 ORGANISM: Bos taurus
 FEATURE: ;
 US-09-511-477-1

Db 3293 ATGCAGTCCCTCCGCCATCGCAGTCAGTCTGACTCTGGCCCTCTCCATCCCCACTTA 3352

Qy 21 ArgArgLeuGluHisThr--PheValPheLeuArgAsnPheSerLeuMetLeuLeu
 DB: 3353 CATAGACTGAGACATACITGTTCTTCTTCTTCAAGCCCTGATCTTIA 3409

RESULT 14
 US-09-025-769B-274/c
 ; Sequence 274, Application US/09025769B
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilaq, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon

APPLICANT: Blueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUNCECS: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27-794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 274:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2755 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLLOGY: circular
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic vector"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..509
 OTHER INFORMATION: /product= "gillip ss, myc tag, amber"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: complement (1853..2509)
 OTHER INFORMATION: /product= "cat resistance"
 US-09-025-769B-274
 Alignment Scores:
 Pred. No.: 65.3
 Score: 61.50
 Percent Similarity: 52.83%
 Best Local Similarity: 28.30%
 Query Match: 20.03%
 DB: 3
 Length: 2755
 Matches: 15
 Conservative: 13
 Mismatches: 8
 Indels: 17
 Gaps: 3
 US-10-031-158-14 (1-58) x US-09-025-769B-274 (1-2755)
 Qy 2 GluMetPheProSerProLeuPhePhePheLeuGlnLeuLeuIleGlnSerSerArg 21
 Db 602 CAGGCCGGCCCCCCCCCCCT-----TTAAATAACGGCAGACAAA 561
 Qy 22 ArgLeuGluLysThrPheValPheLeuArgAsnPheSer----- 34
 Db 560 AAAATGTCGCAAT-----CTGCGCCATTTCATTCACAGGTCAAGCTTATCA 510
 Qy 35 ---IeuMetIleLeuArgTrpIleGlyAlaLysIleArg 46
 Db 509 AGACTCTTATTACCGAGTAGTGTAGCAAGCTAGAAA 471
 RESULT 15
 US-09-490-070A-274/C
 ; Sequence 274, Application US/09490070A
 ; Patent No. 6696248

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pback, Peter
 Ilag, Vic
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman
 White & McAuliffe
 STREET: 1666 K Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,070A
 FILING DATE: 24-Jan-2000
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31-288
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2020
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 274:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2755 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLLOGY: circular
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic vector"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..509
 OTHER INFORMATION: /product= "gillip ss, myc tag, amber"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: complement (1853..2509)
 OTHER INFORMATION: /product= "cat resistance"
 OTHER INFORMATION: /SEQUENCE DESCRIPTION: SEQ ID NO: 274:
 US-09-490-070A-274
 Alignment Scores:
 Pred. No.: 65.3
 Score: 61.50
 Percent Similarity: 52.83%
 Best Local Similarity: 28.30%
 Query Match: 20.03%
 DB: 4
 Length: 2755
 Matches: 15
 Conservative: 13
 Mismatches: 8
 Indels: 17
 Gaps: 3
 US-10-031-158-14 (1-58) x US-09-490-070A-274 (1-2755)
 Qy 2 GluMetPheProSerProLeuPhePhePheLeuGlnLeuLeuIleGlnSerSerArg 21
 Db 602 CAGGCCGGCCCCCCCCCCCT-----TTAAATAACGGCAGACAAA 561
 Qy 22 ArgLeuGluLysThrPheValPheLeuArgAsnPheSer----- 34
 Db 560 AAAATGTCGCAAT-----CTGCGCCATTTCATTCACAGGTCAAGCTTATCA 510

QY 35 --LeuMetLeuLeuArgTyrlleGlyLysBarg 46
Db 509 AGACTCTTATTAACGCAGTAGTTGAAACGTAGAAA 471

RESULT 16
; Sequence 274, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Jining
; Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490, 153
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/025, 769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 2755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic vector"
FEATURE:
NAME/KEY: CDS
LOCATION: 3..509
OTHER INFORMATION: /product= "gIIIIP ss, myc tag, amber
codon"

FEATURE:
NAME/KEY: CDS
LOCATION: complement (1853..2509)
OTHER INFORMATION: /product= "cat resistance"
SEQUENCE DESCRIPTION: SEQ ID NO: 274;
US-09-490-153-274

Alignment Scores:
Pred. No.: 65.3 Length: 2755
Score: 61.50 Matches: 15
Percent Similarity: 55.83% Conservative: 13
Best Local Similarity: 28.30% Mismatches: 8
Query Match: 20.03% Indels: 17
DB: 4 Gaps: 3

US-10-031-158-14 (1-58) x US-09-250-609-79 (1-339)
RESULT 17
; Sequence 79, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383_0210002
; CURRENT APPLICATION NUMBER: US/09/250, 609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 79
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-250-609-79

Alignment Scores:
Pred. No.: 65.3 Length: 339
Score: 61.00 Matches: 18
Percent Similarity: 48.94% Conservative: 5
Best Local Similarity: 38.30% Mismatches: 14
Query Match: 19.87% Indels: 10
DB: 4 Gaps: 2

US-10-031-158-14 (1-58) x US-09-250-609-79 (1-339)
QY 13 LeugInleuLeuLys----GlnPheSerArgArgLeuGluHisthrPheValPheLeu 30
Db 197 CTCCAGTGTTAGAACGCCAGACAGGGGGAGATT----- 235
QY 31 ArgAsnThrSerLeuMetLeuLeuArgTyrlleGlyLysBarg 50
Db 236 ---ASCTTCGGCTTCTAGCTGCTAAGGTGAGAGAGAAATGTCCTCGGCCGGTGC 292
QY 51 TTPASPRProArgArgGlyThr 57
Db 293 TGGCAGCCAAAGAGAGGCACT 313

RESULT 18
US-09-250-611-79
; Sequence 79, Application US/09250611
; Patent No. 6528283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Basset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383_0210001
; CURRENT APPLICATION NUMBER: US/09/250, 611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 79
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-250-611-79

Alignment Scores:

Pred. No.: 3.99
Score: 61.00
Percent Similarity: 48.94%
Best Local Similarity: 38.30%
Query Match: 19.87%
DB: 4

Length: 339
Matches: 18
Conservative: 5
Mismatches: 14
Indels: 10
Gaps: 2

US-10-031-158-14 (1-58) x US-09-250-611-79 (1-339)

Qy 13 LeuGlnIleLeuLeuLys----GlnSerSerArgArgLeuGluHisthrPheValPheLeu 30
Db 197 CTCCAGCTTGATGAGGCCTGAGAGGGAGAAGATT----- 235

Qy 31 ArgAsnPheSerLeuMetLeuLeuArgTyrIleGlyLysLysBargArgAlaThrArgPhe 50
Db 236 --AGCTCGGGCTGAGGTGCTAAGGTGGAAAGAAATTGTCACTCTGCCAGGTGC 292

Qy 51 TTDASPRArgArgGlyThr 57
Db 293 TGGCAGGCCAAAGAGGCACT 313

RESULT 19
US-09-250-609-91
; Sequence 91, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 91
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-250-609-91

Alignment Scores:
Pred. No.: 5.02 Length: 399
Score: 61.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4
Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-609-91 (1-399)

Qy 31 ArgAsnPheSerLeuMetLeuLeuArgTyrIleGlyLysLysBargArgAlaThrArgPhe 50
Db 227 AAGGCTTCGGGCTGAGCTTGCTAAGGTGGAAATTGTCACTCTGCCAGGTGC 286

Qy 51 TTDASPRArgArgGlyThr 57
Db 287 TGGCAGGCCAAAGAGGCACT 307

RESULT 20
US-09-250-611-91
; Sequence 91, Application US/09250611
; Patent No. 6520283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 91
; LENGTH: 399
; TYPE: DNA

US-09-250-611-91
; Sequence 89, Application US/09250611
; Patent No. 6520283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Basset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 89
; LENGTH: 420
; TYPE: DNA

RESULT 21
US-09-250-609-89
; Sequence 89, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 89
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-250-609-89

Alignment Scores:
Pred. No.: 5.4 Length: 420
Score: 61.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4
Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-609-89 (1-420)

Qy 31 ArgAsnPheSerLeuMetLeuLeuArgTyrIleGlyLysLysBargArgAlaThrArgPhe 50
Db 230 AAGGCTTCGGGCTGAGCTTGCTAAGGTGGAAATTGTCACTCTGCCAGGTGC 289

Qy 51 TTDASPRArgArgGlyThr 57
Db 290 TGGCAGGCCAAAGAGGCACT 310

RESULT 22
US-09-250-611-89
; Sequence 89, Application US/09250611
; Patent No. 6520283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Basset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 89
; LENGTH: 420
; TYPE: DNA

; ORGANISM: Homo sapiens
; US-09-250-611-89

Alignment Scores:
Pred. No.: 5.4 Length: 420
Score: 61.00 Matches: 12
Percent Similarity: 53.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-611-89 (1-420)

Qy 31 ArgAsnPheSerLeuMetLeuLeuArgTyrIleGlyLysLysArgArgAlaThrArgPhe 50
Db 230 ArgAGCTTCGGCTGAGCTTGCTAAAGGGAGAAGAATGTCACTCTGCCAGGTGC 289

Qy 51 TTPASPROArgArgLYThr 57
Db 290 TGGCAGCCAAAGAGGACT 310

RESULT 23

US-09-250-609-77 Application US/09250609A

; Sequence 77, Application US/09250609A
; Patent No. 6448943

GENERAL INFORMATION:

APPLICANT: Byrne, Jennifer A.

TITLE OF INVENTION: Members of the D52 Gene Family

FILE REFERENCE: 1383_0210002 CURRENT APPLICATION NUMBER: US/09/250,609A

CURRENT FILING DATE: 1999-02-17 NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 77

TYPE: DNA

ORGANISM: Homo sapiens

; US-09-250-609-77

Alignment Scores:
Pred. No.: 5.47 Length: 424
Score: 61.00 Matches: 12
Percent Similarity: 53.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-609-77 (1-424)

Qy 31 ArgAsnPheSerLeuMetLeuLeuArgTyrIleGlyLysLysArgArgAlaThrArgPhe 50
Db 239 ArgAGCTTCGGCTGAGCTTGCTAAAGGGAGAAGAATGTCACTCTGCCAGGTGC 298

Qy 51 TTPASPROArgArgLYThr 57
Db 299 TGGCAGCCAAAGAGGACT 319

RESULT 25

US-09-250-609-90 Application US/09250609A

; Sequence 90, Application US/09250609A
; Patent No. 6458943

GENERAL INFORMATION:

APPLICANT: Byrne, Jennifer A.

TITLE OF INVENTION: Members of the D52 Gene Family

FILE REFERENCE: 1383_0210002 CURRENT APPLICATION NUMBER: US/09/250,609A

CURRENT FILING DATE: 1999-02-17 NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 90

TYPE: DNA

ORGANISM: Homo sapiens

; US-09-250-609-90

Alignment Scores:
Pred. No.: 6.35 Length: 471
Score: 61.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-609-90 (1-471)

Qy 31 ArgAsnPheSerLeuMetLeuLeuArgTyrIleGlyLysLysArgArgAlaThrArgPhe 50
Db 248 ArgAGCTTCGGCTGAGCTTGCTAAAGGGAGAAGAATGTCACTCTGCCAGGTGC 307

Qy 51 TTPASPROArgArgLYThr 57
Db 308 TGGCAGCCAAAGAGGACT 328

RESULT 26

US-09-250-611-90 Application US/09250611

; Sequence 90, Application US/09250611
; Patent No. 6528283

GENERAL INFORMATION:

APPLICANT: Byrne, Jennifer A.

TITLE OF INVENTION: Members of the D52 Gene Family

FILE REFERENCE: 1383_0210001 CURRENT APPLICATION NUMBER: US/09/250,611

CURRENT FILING DATE: 1999-02-17 NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 90

TYPE: DNA

; LENGTH: 471

```

; ORGANISM: Homo sapiens
US-09-250-611-90

Alignment Scores:
Pred. No.: 6.35 Length: 471
Score: 61.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-611-90 (1-471)
RESULT 27
US-09-250-609-95
; Sequence 95, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.021.0002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 95
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-250-609-95

Alignment Scores:
Pred. No.: 7.71 Length: 540
Score: 61.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 19.87% Indels: 0
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-250-609-95 (1-540)
RESULT 28
US-09-250-611-95
; Sequence 95, Application US/09250611
; Patent No. 6528283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.021.0001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 95
; LENGTH: 540
; TYPE: DNA

Alignment Scores:
Pred. No.: 14.3 Length: 836
Score: 61.00 Matches: 17
Percent Similarity: 65.52% Conservative: 2
Best Local Similarity: 58.62% Mismatches: 9
Query Match: 19.87% Indels: 1
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-495-050A-103 (1-836)
RESULT 29
US-09-495-050A-103/C
; Sequence 103, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED =
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495, 050A
; CURRENT FILING DATE: 2000-01-31
; PRIORITY APPLICATION NUMBER: FEBRUARY 6/118 318
; PRIORITY FILING DATE: FEBRUARY 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO: 103
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 1331917CTI
; US-09-495-050A-103

Alignment Scores:
Pred. No.: 14.3 Length: 836
Score: 61.00 Matches: 17
Percent Similarity: 65.52% Conservative: 2
Best Local Similarity: 58.62% Mismatches: 9
Query Match: 19.87% Indels: 1
DB: 4 Gaps: 0

US-10-031-158-14 (1-58) x US-09-495-050A-103 (1-836)
RESULT 30
US-09-587-184-1/C
; Sequence 1, Application US/09587184
; Patent No. 6479729
; GENERAL INFORMATION:
; APPLICANT: Camochiaro, Peter A.
; APPLICANT: Zack, Donald J.
; TITLE OF INVENTION: Mouse Model for Ocular Neovascularization
; FILE REFERENCE: 001107.00011

```


RESULT 37 US-08-943-731-7/c Sequence 7, Application US/08943731
 Patent No. 6265157 GENERAL INFORMATION:
 APPLICANT: PROCKOP, DARWIN J.
 APPLICANT: SPOTILA, LORETTA D.
 APPLICANT: DELTAS, CONSTANTINOS D.
 APPLICANT: SEREDA, LARISA W.
 APPLICANT: PACK, MICHAEL
 APPLICANT: COLIGE, ALAIN
 APPLICANT: EARLY, JAMES
 APPLICANT: KORKKO, JARMO
 APPLICANT: ALA-KOKKO, LEENA, et al.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
 NUMBER OF SEQUENCES: 666
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
 CITY: PHILADELPHIA
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-7086
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/943, 731
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212, 322
 FILING DATE: 14-MAR-1994
 PRIORITY DATA:
 REFERENCE/DOCKET NUMBER: 9598-27
 ATTORNEY/AGENT INFORMATION:
 NAME: DOYLE LEARY Ph. D., KATHRYN
 REGISTRATION NUMBER: 36,317
 REFERENCE/DOCKET NUMBER: 9598-27
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-965-1284
 TELEFAX: 215-567-2991
 TELEX: 831-494
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1463 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ; US-08-943-731-7
 Alignment Scores:
 Pred. No.: 37.5 Length: 1463
 Score: 60.50 Matches: 17
 Percent Similarity: 42.86% Conservative: 4
 Best Local Similarity: 34.69% Mismatches: 15
 Query Match: 19.71% Indels: 13
 DB: 3 Gaps: 1
 ; US-10-031-158-14 (1-58) x US-08-943-731-7 (1-1463)
 QY 4 PheProProSerProLeuPhePhePheLeuGlnIleLeuIysGlnSerSerArgArgLeu 23
 Db 1366 TTCCGGCCCTCCCCGTCCTCTTCATTCTAAAGCTGCCTGCCTCAT 1307
 24 Glutib-----ThrRheValPheLeu 30

RESULT 38 US-08-943-731-1/c Sequence 1, Application US/08943731
 Patent No. 6265157 GENERAL INFORMATION:
 APPLICANT: PROCKOP, DARWIN J.
 APPLICANT: SPOTILA, LORETTA D.
 APPLICANT: DELTAS, CONSTANTINOS D.
 APPLICANT: SEREDA, LARISA W.
 APPLICANT: PACK, MICHAEL
 APPLICANT: COLIGE, ALAIN
 APPLICANT: EARLY, JAMES
 APPLICANT: KORKKO, JARMO
 APPLICANT: ALA-KOKKO, LEENA, et al.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
 NUMBER OF SEQUENCES: 666
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
 CITY: PHILADELPHIA
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-7086
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/943, 731
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212, 322
 FILING DATE: 14-MAR-1994
 PRIORITY DATA:
 REFERENCE/DOCKET NUMBER: 9598-27
 ATTORNEY/AGENT INFORMATION:
 NAME: DOYLE LEARY Ph. D., KATHRYN
 REGISTRATION NUMBER: 36,317
 REFERENCE/DOCKET NUMBER: 9598-27
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-965-1284
 TELEFAX: 215-567-2991
 TELEX: 831-494
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18609 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ; US-08-943-731-1
 Alignment Scores:
 Pred. No.: 1.38e+03 Length: 18609
 Score: 60.50 Matches: 17
 Percent Similarity: 42.86% Conservative: 4
 Best Local Similarity: 34.69% Mismatches: 15
 Query Match: 19.71% Indels: 13
 DB: 3 Gaps:

US-10-031-158-14 (1-58) x US-08-943-731-1 (1-18609)

Qy 4 PheProProSer-ProLeuPhePheLeuGlnLeuLeuLysGlnSerSerArgArgLeu 23 ; SEQ ID NO 1 ; LENGTH: 9840 ;
; TYPE: DNA ;
; ORGANISM: Mouse ;
Db 1888 TCCCCGCCCTCCCTCCCCGGTCTCTTCCTCAATCTTAAAGCTGCTGCTCTCAT 1829 ; US-09-534-638-1

Qy 24 GluHis---ThrPheValPheLeu 30 ;
Db 1828 CAGCGCGGGTACAGGCCGAGGCCAGGGAGGCTGACTCTTCAGTCTC 1769 ;
Qy 31 ArgAsnPheSerLeuMetLeuIeurg 39 ;
Db 1768 AGGAATTAAAGCAAAGCTTACGTCGC 1742 ;

RESULT 39

US-09-543-681A-392

; Sequence 392, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543.681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIORITY FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 392

; LENGTH: 2715

; ORGANISM: Proteus mirabilis

; US-09-543-681A-392

Alignment Scores:

Pred. No.: 662 ;
Score: 60.00 ;
Percent Similarity: 39.06% ;
Best Local Similarity: 28.12% ;
Query Match: 19.54% ;
DB: 3 ;
Gaps: 1 ;
Length: 9840 ;
Matches: 18 ;
Conservative: 7 ;
Mismatches: 27 ;
Indels: 12 ;

US-10-031-158-14 (1-58) x US-09-534-638-1 (1-9840)

Qy 2 GluMetPheProProSer-ProLeuPhePheLeuGlnLeuLeuLysGlnSerSerArg 21 ;
Db 1041 CAGTGTTCCTCCACCTCTCCATGTGCTTATTCCTACTCTGCTTACCAACACAA 1100 ;
Qy 22 ArgLeuGluHisThrPheValPheLeuIeurgArgSer 34 ;
Db 1101 CAAAAAGCAAAACTCTGAGGTTGAACTCTTCAAAATCTATGGAACT 1160 ;
Qy 35 LeuMetLeuIeurgArgTyrlleGlyLysArgGargAlaThrArg 49 ;
Db 1161 CATTCCCTCTGACTTCCTTAGCTCTAGCTGAGTGCGGTCTCCACTAGG 1220 ;
Qy 50 PheTrpAspPro 53 ;
Db 1221 CCCTGGAACT 1232 ;

Search completed: December 8, 2004, 09:20:25

Job time : 71 secs

RESULT 40

US-09-534-638-1

; Sequence 1, Application US/09534638

; Patent No. 6320038

; GENERAL INFORMATION:

; APPLICANT: Pertti A.J.

; APPLICANT: Brandt, Anniika

; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof

; TITLE OF INVENTION: For therapy and diagnosis

; FILE REFERENCE: 2530-104

; CURRENT APPLICATION NUMBER: US/09/534,638

; EARLIER APPLICATION NUMBER: 09/365755

; EARLIER FILING DATE: 1999-08-03

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2004, 08:54:21 ; Search time 271 Seconds

(without alignments) 1.80.016 Million cell updates/sec

Title: US-10-031-158-14

Perfect score: 307

Sequence: 1 MQMPPPSPLFFFLQLLKQSS.....RYIGKRRATRFWDPRRGTP 58

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4085731 seqs, 2756760397 residues

Total number of bits satisfying chosen parameters: 8171462

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEU=f,frame+_p2n.model -DEV=x1h

-Q=/sgn2_1/USPRO_spool/US0031158/runat_06122004_082701_16006/app_query.fasta_1.199

-DB=Published Applications NA -OPFM=rfastap -SUFFIX=rnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPTEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62

-TRANS=human40-cdd1 -LIST=45 -DOCALL=200 -THR SCORE=PCT -THR MAX=100

-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=PTO -NORM=ext -HEARSIZE=500 -MINLN=0

-MAXLEN=200000000 -USER=US1031158 @CGN 1_1 354 @runat_06122004_082701_16006

-NCPU=6 -ICFU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSEPBLOCK=100

-LONGLOG -DEV TIMEOUT=120 -WARM TIMEOUT=30 -THREADS=1 -XGAROP=10 -XGABEXT=.5

-FGAPOP=6 -FGATPEXT=7 -YGAPOP=10 -YGABEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA: *

1: /cgnd_6/ptodata_1/pubpna/us07_PUBCOMB.seq: *

2: /cgnd_6/ptodata_1/pubpna/PCT NEW PUB. seq: *

3: /cgnd_6/ptodata_1/pubpna/us06_PUBCOMB.seq: *

4: /cgnd_6/ptodata_1/pubpna/us07_NEW PUB. seq: *

5: /cgnd_6/ptodata_1/pubpna/PCTUS_PUBCOMB.seq: *

6: /cgnd_6/ptodata_1/pubpna/us08_NEW PUB. seq: *

7: /cgnd_6/ptodata_1/pubpna/us08_PUBCOMB.seq: *

8: /cgnd_6/ptodata_1/pubpna/us09_PUBCOMB.seq: *

9: /cgnd_6/ptodata_1/pubpna/us09_PUBCOMB.seq: *

10: /cgnd_6/ptodata_1/pubpna/us09_PUBCOMB.seq: *

11: /cgnd_6/ptodata_1/pubpna/us09C_PUBCOMB.seq: *

12: /cgnd_6/ptodata_1/pubpna/us09 NEW PUB. seq: *

13: /cgnd_6/ptodata_1/pubpna/us10_PUBCOMB.seq: *

14: /cgnd_6/ptodata_1/pubpna/us10C_PUBCOMB.seq: *

15: /cgnd_6/ptodata_1/pubpna/us10C_PUBCOMB.seq: *

16: /cgnd_6/ptodata_1/pubpna/us10_PUBCOMB.seq: *

17: /cgnd_6/ptodata_1/pubpna/us10E_PUBCOMB.seq: *

18: /cgnd_6/ptodata_1/pubpna/us10 NEW PUB. seq: *

19: /cgnd_6/ptodata_1/pubpna/us11_NEW PUB. seq: *

20: /cgnd_6/ptodata_1/pubpna/us60 NEW PUB. seq: *

21: /cgnd_6/ptodata_1/pubpna/us60_PUBCOMB.seq: *

Result No.	Score	Query	Length	DB	ID	Description	
1	307	100.0	470	9	US-09-864-761-15428	Sequence 15428, A	
2	307	100.0	477	9	US-09-864-761-15438	Sequence 15438, A	
3	307	100.0	825	15	US-10-340-536-29	Sequence 404, App	
4	307	100.0	1027	15	US-10-205-823-40	Sequence 23, App	
5	307	100.0	1395	18	US-10-643-795A-23	Sequence 16, App	
6	307	100.0	1418	10	US-09-957-708-16	Sequence 31943, A	
7	302	98.4	316	9	US-09-864-761-31943	Sequence 317, App	
8	294	95.8	1421	9	US-10-101-510-492	Sequence 676, App	
9	294	95.8	1799	15	US-10-101-510-492	Sequence 424, App	
10	284	92.5	1586	10	US-09-960-706-676	Sequence 58, App	
11	284	92.5	1586	10	US-09-873-319-24	Sequence 10505, A	
12	245	79.8	1155	9	US-09-925-300-58	Sequence 10504, A	
13	75	24.4	1813	17	US-10-437-963-35632	Sequence 136731, A	
14	73.5	23.9	13	US-10-027-632-136731	Sequence 10550, A		
15	73.5	23.9	15	US-10-027-632-10230	Sequence 10230, A		
16	72.5	23.6	618	13	US-10-027-632-105504	Sequence 6393, A	
17	72.5	23.6	618	13	US-10-027-632-105504	Sequence 136730, A	
18	72.5	23.6	618	15	US-10-027-632-136730	Sequence 136730, A	
19	72.5	23.6	353	16	US-10-424-599-127254	Sequence 127254, A	
20	72.5	23.6	27118	10	US-09-764-891-22460	Sequence 22460, A	
21	21	23.6	72.5	1718	15	US-10-205-428-428-1018	Sequence 3211, App
22	21	23.3	328	16	US-10-424-599-63943	Sequence 203503, A	
23	23	23.0	618	13	US-10-027-632-136730	Sequence 203503, A	
24	23	20.5	618	15	US-10-027-632-136730	Sequence 203503, A	
25	25	69.5	22.6	353	16	US-10-424-599-127254	Sequence 203503, A
26	69.5	22.6	2145	16	US-10-282-122A-22460	Sequence 203503, A	
27	69.5	22.6	2241	9	US-09-881-752A-321	Sequence 203503, A	
28	68.5	22.3	585	13	US-10-027-632-203503	Sequence 203503, A	
29	68.5	22.3	585	15	US-10-027-632-203503	Sequence 203503, A	
30	67.5	22.0	535	18	US-10-363-335-15080	Sequence 256, App	
31	67.5	22.0	942	9	US-09-962-832-256	Sequence 1338, App	
32	67.5	22.0	1037	16	US-10-342-887-1338	Sequence 1338, App	
33	67.5	22.0	2532	10	US-09-918-624B-4	Sequence 4, App	
34	67.5	22.0	11838	10	US-09-764-891-0202	Sequence 7020, App	
35	67.5	22.0	11838	15	US-10-311-455-115	Sequence 1165, App	
36	67.5	22.0	13814	15	US-10-425-115-936	Sequence 4936, App	
37	67.5	22.0	314	18	US-10-425-115-936	Sequence 4936, App	
38	67	21.8	1265	13	US-10-077-632-252580	Sequence 252580, App	
39	67	21.8	1265	15	US-10-077-632-252580	Sequence 252580, App	
40	67	21.8	1265	15	US-10-425-115-128054	Sequence 128054, App	
41	67	21.8	1726	18	US-10-425-115-128054	Sequence 128054, App	
42	67	21.8	29829	13	US-10-87-192-694	Sequence 694, App	
43	67	21.8	3673778	15	US-10-312-81-2	Sequence 2, App	
44	66.5	21.7	328	16	US-10-424-599-134189	Sequence 134189, App	
45	66.5	21.7	1316	18	US-10-425-115-135505	Sequence 135505, App	

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Db 332 ATGGCAAGAAGAAGAGGACACGATTCTGGATCCACGGGGACACCA 385
 RESULT 3
 US-10-340-536-29
 ; Sequence 29, Application US/10340536
 ; Publication No. US200317512A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Rebecca
 ; APPLICANT: Born, Willi
 ; APPLICANT: Roark, Christina
 ; APPLICANT: Aydinoglu, M. Kemal
 ; TITLE OF INVENTION: Use of Soluble Gamma Delta T Cell Receptors for Regulating T Cell
 ; TITLE OF INVENTION: Function
 ; FILE REFERENCE: 2879-89
 ; CURRENT APPLICATION NUMBER: US/10/340,536
 ; CURRENT FILING DATE: 2003-01-10
 ; PRIOR APPLICATION NUMBER: 60/347,285
 ; PRIOR FILING DATE: 2002-03-05
 ; NUMBER OF SEQ ID NOS: 455
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 404
 ; LENGTH: 1027
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-340-536-29
 Alignment Scores:
 Pred. No.: 1.11e-35 Length: 825
 Score: 307.00 Matches: 58
 Percent Similarity: 100.00% Conservative: 58
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0
 US-10-340-536-29 (1-825)
 QY 1 MetGlnMetPheProProSerProLeuPhePhePhePheLeuGlnLeuLeuIleGlnSerSer 20
 Db 440 ATGCAGATGTTCCCCAAAGCCACTATTTCCTTCATTGGTGAACAAAGCTC 499
 QY 21 ArgArgLeuGluIleThrPheLeuIleArgAsnPhesSerLeuMetLeuLeuArgTyr 40
 Db 500 AGAACGCTGGACATACCTTGCTCTCTGAGAAATTTCCTGTGATTTAGATAC 559
 QY 41 IleGlyLysIleSarGargAlaThrArgPhePheProGlyArgLysPro 58
 Db 560 ATTGGAGAGAAAGAGAGCACACGATTCTGGATCCACGGAGGGACACCA 613
 RESULT 4
 US-10-205-823-404
 ; Sequence 404, Application US/10205823
 ; Publication No. US20030108963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHLEEL, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Corbatcheva, Bella
 ; APPLICANT: Hoerich, Sebastian
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Nonsey, Angela M.
 ; APPLICANT: Giatt, Karen
 ; APPLICANT: Anderson, Dustin
 ; APPLICANT: Zhao, Xumei
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR THE DIAGNOSIS AND
 ; TITLE OF INVENTION: TREATMENT OF TUMOR
 ; FILE REFERENCE: P50261-US
 ; CURRENT APPLICATION NUMBER: US/10/643,795A
 ; CURRENT FILING DATE: 2003-08-19
 ; PRIOR APPLICATION NUMBER: US 60/404,809
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/405,645
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/413,192
 ; PRIOR FILING DATE: 2002-09-23
 ; PRIOR APPLICATION NUMBER: US 60/419,008
 ; PRIOR FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/426,847
 ; PRIOR FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US 60/484,959
 ; PRIOR FILING DATE: 2003-07-02
 ; NUMBER OF SEQ ID NOS: 158
 ; SEQ ID NO: 23
 ; LENGTH: 1395
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 RESULT 5
 US-10-643-795A-23
 ; Sequence 23, Application US/10643795A
 ; Publication No. US20040241703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FREDERIC J. DESAUVAGE
 ; APPLICANT: GRETCHEN FRANTZ
 ; APPLICANT: KENNETH J. HILLIAN
 ; APPLICANT: PAUL POLAKIS
 ; APPLICANT: ANDREW POISON
 ; APPLICANT: VICTORIA SMITH
 ; APPLICANT: SUSAN D. SPENCER
 ; APPLICANT: THOMAS D. WU
 ; APPLICANT: ZEMIN ZHANG
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TITLE OF INVENTION: TREATMENT OF TUMOR
 ; FILE REFERENCE: P50261-US
 ; CURRENT APPLICATION NUMBER: US/10/643,795A
 ; CURRENT FILING DATE: 2003-08-19
 ; PRIOR APPLICATION NUMBER: US 60/404,809
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/405,645
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/413,192
 ; PRIOR FILING DATE: 2002-09-23
 ; PRIOR APPLICATION NUMBER: US 60/419,008
 ; PRIOR FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/426,847
 ; PRIOR FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US 60/484,959
 ; PRIOR FILING DATE: 2003-07-02
 ; NUMBER OF SEQ ID NOS: 158
 ; SEQ ID NO: 23
 ; LENGTH: 1395
 ; TYPE: DNA
 ; ORGANISM: Homo sapien

RESULT 8
US-09-954-456-317
; Sequence 317, Application US/09954456
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
TITLE OF INVENTION: Processes for Identifying Anti-Cancer Therapeutic Agents Using Candi
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
PRIORITY FILING DATE: 2001-09-18
PRIORITY APPLICATION NUMBER: US/60/233,617
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US/60/234,052
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: US/60/234,923
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,134
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,637
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,638
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,711
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,720
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,840
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,863
PRIORITY FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 492
LENGTH: 1799
SBQ ID NO: 492
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-492
Alignment Scores:
Pred. No.: 2.05e-33 Length: 1421
Score: 294.00 Matches: 55
Percent Similarity: 98.28% Conservative: 2
Best Local Similarity: 94.83% Mismatches: 1
Query Match: 95.77% Indels: 0
DB: GCGAAGAAAAGAGAGACACAGATCTGGGATCCAGGGAGAACACCA 172
RESULT 9
US-10-101-510-492
; Sequence 422, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIORITY APPLICATION NUMBER: 6/0/276,947
PRIORITY FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentin Ver. 2.1
SBQ ID NO: 492
LENGTH: 1799
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-492
Alignment Scores:
Pred. No.: 2.84e-33 Length: 1799
Score: 294.00 Matches: 58
Percent Similarity: 98.31% Conservative: 0
Best Local Similarity: 98.31% Mismatches: 0
Query Match: 95.77% Indels: 1
DB: GCGAAGAAAAGAGAGACACAGATCTGGGATCCAGGGAGAACACCA 171
RESULT 10
US-09-960-706-676
; Sequence 676, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munzer, William E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIORITY APPLICATION NUMBER: 6/0/223,323
PRIORITY FILING DATE: 2000-08-07
PRIORITY APPLICATION NUMBER: 09/873,319
PRIORITY FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 676
LENGTH: 1586
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134280A1 M30894
US-09-960-706-676
Alignment Scores:
Pred. No.: 7.43e-32 Length: 1586
Score: 284.00 Matches: 53
Percent Similarity: 96.55% Conservative: 3
Best Local Similarity: 96.55% Mismatches: 3
Query Match: 96.55% Indels: 3
DB: AGGGCTGGAACATACCTTGTCCTGAGAAATTTCGAGATAATTTAGATAC 542
RESULT 11
US-09-960-706-676
; Sequence 423, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munzer, William E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIORITY APPLICATION NUMBER: 6/0/223,323
PRIORITY FILING DATE: 2000-08-07
PRIORITY APPLICATION NUMBER: 09/873,319
PRIORITY FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 676
LENGTH: 1586
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134280A1 M30894
US-09-960-706-676
Alignment Scores:
Pred. No.: 7.43e-32 Length: 1586
Score: 284.00 Matches: 53
Percent Similarity: 96.55% Conservative: 3
Best Local Similarity: 96.55% Mismatches: 3
Query Match: 96.55% Indels: 3
DB: ATGGCAGAAGAGAGACACAGATCTGGGATCCAGGGAGAACACCA 596
RESULT 12
US-09-960-706-676
; Sequence 423, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munzer, William E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIORITY APPLICATION NUMBER: 6/0/223,323
PRIORITY FILING DATE: 2000-08-07
PRIORITY APPLICATION NUMBER: 09/873,319
PRIORITY FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 676
LENGTH: 1586
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134280A1 M30894
US-09-960-706-676
Alignment Scores:
Pred. No.: 7.43e-32 Length: 1586
Score: 284.00 Matches: 53
Percent Similarity: 96.55% Conservative: 3
Best Local Similarity: 96.55% Mismatches: 3
Query Match: 96.55% Indels: 3
DB: ATGGCAGAAGAGAGACACAGATCTGGGATCCAGGGAGAACACCA 596

Query Match: 92.51% Indels: 0 Gaps: 0 DB:

US-10-031-158-14 (1-58) x US-09-960-706-676 (1-1586)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
Db 553 ATGCAGATGTTCGCCAAGCCACTATTCTCTCTGATGCTGAAAGAACCTCC 612

QY 21 ArgArgLeuGluHisthPheValPheLeuArgAsnSerLeuLeuLeuArgTyr 40
Db 613 AGAGGCTGGAACATATCTTGCTCTGAGAATTCTCCAGGAGATTTAGATAC 672

RESULT 11

US-09-873-319-424

; Sequence 424, Application US/09873319A

; Publication No. US20030134324A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; APPLICANT: Kulkarni, Prakash

; APPLICANT: Gerzenberg, Robert H.

; APPLICANT: Waga, Iwao

; APPLICANT: Yamamoto, Jun

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using Gene Expression Profile

; FILE REFERENCE: 44931-5029-US

; CURRENT APPLICATION NUMBER: US/09/873,319A

; CURRENT FILING DATE: 2001-06-05

; EARLIER APPLICATION NUMBER: US 60/223,323

; EARLIER FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 755

; SEQ ID NO: 424 LENGTH: 1586

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: OTHER INFORMATION: Genbank Accession No. US20030134324A1 M30894

Alignment Scores:

Pred. No.: 7.43e-32 Score: 284.00 Percent Similarity: 91.38% Best Local Similarity: 91.51% Query Match: 10

Length: 1586 Matches: 53 Conservative: 3 Mismatches: 2 Indels: 0 Gaps: 0

US-09-873-319-424 (1-1586)

US-10-031-158-14 (1-58) x US-09-925-300-58 (1-1155)

Alignment Scores:

Pred. No.: 3.19e-26 Score: 245.00 Percent Similarity: 91.07% Best Local Similarity: 91.07% Query Match: 9

Length: 1155 Matches: 51 Conservative: 0 Mismatches: 5 Indels: 1 Gaps: 0

US-10-031-158-14 (1-58) x US-09-925-300-58 (1-1155)

QY 1 MetGlnMetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSer 20
Db 175 ATGCAGATGTTCGCCAAGCCACTATTCTCTCTGATGCTGAAAGAACCTCC 233

QY 21 ArgArgLeuGluHisthPheValPheLeuArgAsnSerLeuLeuLeuArgTyr 40
Db 234 AGAGGCTGGAACATATCTTGCTCTGAGAATTCTCCAGGAGGCG 341

RESULT 13

US-10-437-963-35632/C

; Sequence 35632, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovacic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO: 35632 LENGTH: 1813

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_39533C.1

RESULT 12

US-09-925-300-58

; Sequence 58, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben,

US-10-437-963-33632

Alignment Scores:
Pred. No.: 1.43 Length: 1813
Score: 75.00 Matches: 24
Percent Similarity: 40.85% Conservative: 5
Best Local Similarity: 33.80% Mismatches: 22
Query Match: 24.43% Indels: 20
DB: 17 Gaps: 3

US-10-031-158-14 (1-58) x US-10-437-963-33632 (1-1813)

QY 5 ProPro-----SerProLeuPhePhePheLeuGlnLeuLeuLeu 17
DB 1740 CGGCCACGGCTTAACTGTGCTTACGCCTTATTTCCTCTCCTGCACTGT 1681

QY 18 GinSerSer------ArgArgLeuLys 25
DB 1680 TCCCTCTCTCTCTCTCTCGCCCTCCACACTGGCACACTCTGTGAACT 1621

QY 26 ThrPheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyrIleGlyLysLysArg 45
DB 1620 CTCCTCTCTGCTCTGGTTAACTCTGCTCTCCATCTCGCGCGATCGA 1564

QY 46 ArgAlaThrArgPheTrpAspProArgArgGly 56
DB 1563 TG GCC ATG GAG GAG GTG GAC GCA AGG AGA GGG 1531

RESULT 14

; Sequence 136731, Application US/10027632
; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027, 632

; PRIOR APPLICATION NUMBER: US 6/0/218, 006
PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 6/0/198, 676
PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 6/0/193, 483
PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 6/0/185, 218
PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 6/0/198, 676
PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 6/0/156, 358
PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 6/0/146, 002
PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 136731
LENGTH: 618
TYPE: DNA
ORGANISM: Human
US-10-027-632-136731

Alignment Scores:
Pred. No.: 0.54 Length: 618
Score: 73.50 Matches: 22
Percent Similarity: 51.72% Conservative: 8
Best Local Similarity: 37.93% Mismatches: 25
Query Match: 23.94% Indels: 3
DB: 15 Gaps: 1

US-10-031-158-14 (1-58) x US-10-027-632-136731 (1-618)

QY 3 MetPheProProSerProLeuPhePhePheLeuGlnSerSerArgArg 22
DB 195 CTATTCCTCCAAACCTGGCTTTTT--GAGACARAGTCTGGCTGGTCACCAAGG 139

QY 23 LeuGluLysThrPheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyrIleGly 42
DB 138 CTGGAGCATAGTAGTGATCTGGCTACTGCAACCTCTGGCTGGTCAAGCCA 79

US-10-027-632-05504/c
; Sequence 105504, Application US/10027632
; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027, 632

; PRIOR APPLICATION NUMBER: US 6/0/218, 006
PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 6/0/167, 363
PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 6/0/193, 483
PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 6/0/185, 218
PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 6/0/198, 676
PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 136731
LENGTH: 618
TYPE: DNA
ORGANISM: Human
US-10-027-632-136731

Alignment Scores:
Pred. No.: 0.54 Length: 618
Score: 73.50 Matches: 22
Percent Similarity: 51.72% Conservative: 8
Best Local Similarity: 37.93% Mismatches: 25
Query Match: 23.94% Indels: 3
DB: 13 Gaps: 1

US-10-031-158-14 (1-58) x US-10-027-632-136731 (1-618)

QY 3 MetPheProProSerProLeuPhePhePheLeuGlnSerSerArgArg 22
DB 78 TCTCCCTCCAGCCCTCCAGGCTAGCTGGGACTACAGGAGGGCCACCA 29

RESULT 16

; Sequence 105504, Application US/10027632
; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027, 632

; PRIOR APPLICATION NUMBER: US 6/0/218, 006
PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 6/0/167, 363
PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 6/0/193, 483
PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 6/0/185, 218
PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 6/0/198, 676
PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 136731
LENGTH: 618
TYPE: DNA
ORGANISM: Human
US-10-027-632-136731

Alignment Scores:
Pred. No.: 0.54 Length: 618
Score: 73.50 Matches: 22
Percent Similarity: 51.72% Conservative: 8
Best Local Similarity: 37.93% Mismatches: 25
Query Match: 23.94% Indels: 3
DB: 13 Gaps: 1

US-10-031-158-14 (1-58) x US-10-027-632-136731 (1-618)

QY 3 MetPheProProSerProLeuPhePhePheLeuGlnSerSerArgArg 22
DB 78 TCTCCCTCCAGCCCTCCAGGCTAGCTGGGACTACAGGAGGGCCACCA 29

FILE REFERENCE: 108827-129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 105504

LENGTH: 618

TYPE: DNA

ORGANISM: Human

US-10-027-632-105505

Alignment Scores:

pred. No.:	0.761	Length:	618
Score:	72.50	Matches:	22
Percent Similarity:	51.72%	Conservative:	8
Best Local Similarity:	37.93%	Mismatches:	25
Query Match:	23.62%	Indels:	3
DB:	13	Gaps:	1

US-10-031-158-14 (1-58) x US-10-027-632-105504 (1-618)

QY 3 MetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSerArgArg 22

Db 195 CTATTCCTCCAAACCTGCTTTTTT--GAGACAAGCTCCTCTGCACCAAGG 139

QY 23 LeuGluHiSThrPheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyRileGly 42

Db 138 CTCGAGCATAGTAGTGATCTGGTCACTGCTCTCGGTCAAAGGAT 79

QY 43 LysLysBargArgGlnSerArgPro--TPASProArgArgGlyThrPro 58

Db 78 TCTCTGCCTCAGCCTCCAAAGTAGCTGGACTCACAGGAGGGGCCACCA 29

RESULT 18

US-10-027-632-105504/c

; Sequence 105504, Application US/10027632

; Publication No. US2003024075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827-129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 105504

LENGTH: 618

TYPE: DNA

ORGANISM: Human

US-10-027-632-105504

Alignment Scores:

pred. No.:	0.761	Length:	618
Score:	72.50	Matches:	22
Percent Similarity:	51.72%	Conservative:	8
Best Local Similarity:	37.93%	Mismatches:	25
Query Match:	23.62%	Indels:	3
DB:	15	Gaps:	1

US-10-031-158-14 (1-58) x US-10-027-632-105505 (1-618)

QY 3 MetPheProProSerProLeuPhePhePheLeuGlnLeuLeuLysGlnSerSerArgArg 22

Db 195 CTATTCCTCCAAACCTGCTTTTTT--GAGACAAGCTCCTCTGCACCAAGG 139

QY 23 LeuGluHiSThrPheValPheLeuArgAsnProSerLeuMetLeuLeuArgTyRileGly 42

Db 138 CTCGAGCATAGTAGTGATCTGGTCACTGCTCTCGGTCAAAGGAT 79

RESULT 19
US-10-027-632-105505/C
; Sequence 105505, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Title of Invention: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827_129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIORITY APPLICATION NUMBER: US 60/218,006
; PRIORITY FILING DATE: 2000-07-12
; PRIORITY APPLICATION NUMBER: US 60/198,676
; PRIORITY FILING DATE: 2000-04-20
; PRIORITY APPLICATION NUMBER: US 60/193,483
; PRIORITY FILING DATE: 2000-03-29
; PRIORITY APPLICATION NUMBER: US 60/185,218
; PRIORITY FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/167,363
; PRIORITY FILING DATE: 1999-11-23
; PRIORITY APPLICATION NUMBER: US 60/156,358
; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 60/146,002
; PRIORITY FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105505
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-105505

Alignment Scores:
Pred. No.: 0.761 Length: 618
Score: 72.50 Matches: 22
Percent Similarity: 51.72% Conservative: 8
Best Local Similarity: 37.93% Mismatches: 25
Query Match: 23.62% Indels: 3
DB: 15 1 Gaps: 1

RESULT 20
US-10-027-632-105505/C
; Sequence 105505, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Title of Invention: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827_129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIORITY APPLICATION NUMBER: US 60/218,006
; PRIORITY FILING DATE: 2000-07-12
; PRIORITY APPLICATION NUMBER: US 60/198,676
; PRIORITY FILING DATE: 2000-04-20
; PRIORITY APPLICATION NUMBER: US 60/193,483
; PRIORITY FILING DATE: 2000-03-29
; PRIORITY APPLICATION NUMBER: US 60/185,218
; PRIORITY FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/167,363
; PRIORITY FILING DATE: 1999-11-23
; PRIORITY APPLICATION NUMBER: US 60/156,358
; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 60/146,002
; PRIORITY FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105505
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-105505

Alignment Scores:
Pred. No.: 0.761 Length: 618
Score: 72.50 Matches: 22
Percent Similarity: 51.72% Conservative: 8
Best Local Similarity: 37.93% Mismatches: 25
Query Match: 23.62% Indels: 3
DB: 15 1 Gaps: 1

RESULT 21
US-10-205-428-1018/C
; Sequence 1018, Application US/10205428
; Publication No. US2003108907A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA117C1
; CURRENT APPLICATION NUMBER: US/10/205,428
; PRIORITY APPLICATION NUMBER: 09/764,892
; PRIORITY FILING DATE: 2001-01-17
; PRIORITY APPLICATION NUMBER: 60/179,065
; PRIORITY FILING DATE: 2000-01-31
; PRIORITY APPLICATION NUMBER: 60/180,628
; PRIORITY FILING DATE: 2000-02-04
; PRIORITY APPLICATION NUMBER: 60/214,886
; PRIORITY FILING DATE: 2000-06-28
; PRIORITY APPLICATION NUMBER: 60/217,487
; PRIORITY FILING DATE: 2000-07-11
; PRIORITY APPLICATION NUMBER: 60/225,758
; PRIORITY FILING DATE: 2000-08-14
; PRIORITY APPLICATION NUMBER: 60/220,963
; PRIORITY FILING DATE: 2000-07-26
; PRIORITY APPLICATION NUMBER: 60/217,496
; PRIORITY FILING DATE: 2000-07-11
; PRIORITY APPLICATION NUMBER: 60/225,447
; PRIORITY FILING DATE: 2000-08-14
; PRIORITY APPLICATION NUMBER: 60/218,290
; PRIORITY FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1019
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 1018
; LENGTH: 27118
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-205-428-1018

Alignment Scores:
Pred. No.: 141 Length: 27118
Score: 72.50 Matches: 19
Percent Similarity: 64.86% Conservative: 5

Alignment Scores:

pred. No.:	1.51	Length:	618
Score:	70.50	Matches:	22
Percent Similarity:	50.00%	Conservative:	7
Best Local Similarity:	37.93%	Mismatches:	26
Query Match:	22.96%	Indels:	3
DB:	15	Gaps:	1

US-10-031-158-14 (1-58) x US-10-027-632-136730 (1-618)

QY 3 MetPheProProSerProLeuPhePhePhePheLeuGluLeuLeuLysGlnSerSerArgArg 22
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
 Db 195 CTATTCACTCCCAAACCTGCCTTTTITTT--GAGACAAGCTCTCKTCCTCACAGG 139
 QY 23 LeuGluHisThrPheValPheLeuArgAsnPheSerLeuMetLeuLeuArgTyrIleGly 42
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
 Db 138 CTGGAGCATAGTAGATGATGATCTGGCTCTGCACCTCTGCTCTGGCTCAACCAAT 79
 QY 43 LysLysArgArgGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGly 58
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
 Db 78 TCTCCCTGCCTCAGCTCCCAAGTAGCTGGACTACAGGAGGGGCCACCA 29

```

; Sequence 321, Application US/09881752A1
; Patent No. US20020115070A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Omer, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1
; TITLE OF INVENTION: Genomic Polypeptides in the
; FILE REFERENCE: 0612/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE: CDS
; LOCATION: (52) . . . (2193)
; US-09-881-752A-321

Alignment Scores:
; Pred. No.: 12.7 Length: 2241
; Score: 69.50 Matches: 25
; Percent Similarity: 51.61% Conservative: 7
; Best Local Similarity: 40.24% Mismatches: 17
; Query Match: 22.64% Indels: 14
; DB: Gaps: 3
; DB: Gaps: 13
; DB: Gaps: 2

US-10-031-158-14 (1-58) x US-09-881-752A-321 (1-2241)

QY          1 MetGlnMetPheProProSerPro--Leu 9
Db 2130 ATACAAATGTCCTCCCTAGCCCTGACTCTCATCTTCAAACCCATATTCTAGCCRT 2071
QY          10 PhePhePheLeuGlnLeuLeuLeuGlySerSerSerArgArgLeuGluHistPheAla 29
Db 2070 GTATTTCCTGCAA---TCAAAAGCAGCAGCTGACTCTCTCTCTCTCTCTCTCTCT 2014
QY          30 LeuArgAsnPheSerLeuMetLeuLeuArgTyrosGlyLysLysArgGalaThrArg 49
Db 2013 TCCAAGCT-TTT---CTAGCTAAATCGTTCAAATCTAGGGTCCGCTCTCTCT 1958
QY          50 PheTrp 51
Db 1957 TTTCGG 1952

RESULT 28
US-10-027-632-203503
; Sequence 203503, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Reference: 108827-129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32520
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 203503
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-203503

Alignment Scores:
; Pred. No.: 2.79 Length: 585
; Score: 68.50 Matches: 18
; Percent Similarity: 49.09% Conservative: 9
; Best Local Similarity: 32.73% Mismatches: 19

```

Query Match: 22.31%
DB: 15 Gaps: 9
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15080
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CPG-island No: 15080
US-10-363-345A-15079
QY 41 RlegIYlylsArgArgAlaThrArgPheTrpAspProArgArg 55
Db 466 GTAGGAAAGAGGAGCTGGCATTTCTTATGTAAACCAAGAAA 510
RESULT 30
US-10-363-345A-15079
QY 41 RlegIYlylsArgArgAlaThrArgPheTrpAspProArgArg 55
Db 466 GTAGGAAAGAGGAGCTGGCATTTCTTATGTAAACCAAGAAA 510
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 15079
LENGTH: 535
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CPG-island No: 15079
Alignment Scores:
Pred. No.: 3.48 Length: 535
Score: 67.50 Matches: 18
Percent Similarity: 55.56% Conservative: 7
Best Local Similarity: 40.00% Mismatches: 15
Query Match: 21.99% Indels: 5
DB:
QY 52 AspProArgArgAla 56
Db 343 -----CCTCGGCGA 335
RESULT 32
US-10-363-345A-15079
QY 12 PheLeuGlnLeuLeuLysGlnSerSerArgArgLeuGluHisThrPheValPheLeuArg 31
Db 82 TTTTTTCATGCGTGGCGG-----CGCGTTAGTTTGCGTTTTTTGCGGG 135
QY 32 AsnPheSerLeuMetLeuLeuArgTyroIleGlyLysLysArgArgAlaThrArgPheTrp 51
Db 136 GTTTGGCTATTTTATTTGGTGGATCCGGTTTCGGTTGTTAGTT-- 192
RESULT 31
US-10-363-345A-15080/C
; Sequence 15080, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 15079
LENGTH: 535
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CPG-island No: 15079
Alignment Scores:
Pred. No.: 3.48 Length: 535
Score: 67.50 Matches: 18
Percent Similarity: 55.56% Conservative: 7
Best Local Similarity: 40.00% Mismatches: 15
Query Match: 21.99% Indels: 5
DB:
QY 12 PheLeuGlnLeuLeuLysGlnSerSerArgArgLeuGluHisThrPheValPheLeuArg 31
Db 454 TTGTTTGCATGCTGAGCGG-----GGCGTTAGTTTGCGTTTTTTGCGGG 401
QY 32 AsnPheSerLeuMetLeuLeuArgTyroIleGlyLysLysArgArgAlaThrArgPheTrp 51
Db 400 GTTTTCGCTTAATTTTTATTTGGTTGGGATCGCGTTGGGTTGGTTGTTAGGTT-- 344
QY 52 AspProArgArgAla 56
Db 343 -----CCTCGGCGA 335
RESULT 32
US-09-962-832-255
; Sequence 256, Application US/09962832
; GENERAL INFORMATION:
; APPLICANT: Eulner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 683290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/335,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 256
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; OS-09-962-832-256
Alignment Scores:
Pred. No.: 7.6 Length: 942
Score: 67.50 Matches: 17
Percent Similarity: 61.11% Conservative: 5
Best Local Similarity: 47.22% Mismatches: 11
Query Match: 21.99% Indels: 3
DB:
QY 21 ArgArgLeuGluHisThrPheLeuArgArgAlaThrArgPheTrpAspProArgArg 39
Db 620 AGACATCTGCTGATACCGCTACTATTTGATGATGTTCCATGCCCTTGACGGGAGA 679
US-10-031-158-14 (1-58) x US-10-027-632-203503 (1-585)
QY 5 ProProSerProLeuPheLeuPheLeuGlnSerSerArgArgLeuGlu 24
Db 361 CCTCCCTCCCCCAGCACTTTTC-----CAATCTCTCTCTCTATGCC 405
QY 25 HisThrPheValPheLeuArgAspSerLeuMetLeuLeu---ArgTyr 40
Db 406 CTACGATTATTTATTTTGTCTACTCTTACCTGACACTGTGACCAATT 465
RESULT 30
US-10-363-345A-15079
QY 41 RlegIYlylsArgArgAlaThrArgPheTrpAspProArgArg 55
Db 466 GTAGGAAAGAGGAGCTGGCATTTCTTATGTAAACCAAGAAA 510
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 15079
LENGTH: 535
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CPG-island No: 15080
US-10-363-345A-15080
Alignment Scores:
Pred. No.: 3.48 Length: 535
Score: 67.50 Matches: 18
Percent Similarity: 55.56% Conservative: 7
Best Local Similarity: 40.00% Mismatches: 15
Query Match: 21.99% Indels: 5
DB:
QY 12 PheLeuGlnLeuLeuLysGlnSerSerArgArgLeuGluHisThrPheValPheLeuArg 31
Db 454 TTGTTTGCATGCTGAGCGG-----GGCGTTAGTTTGCGTTTTTTGCGGG 401
QY 32 AsnPheSerLeuMetLeuLeuArgTyroIleGlyLysLysArgArgAlaThrArgPheTrp 51
Db 400 GTTTTCGCTTAATTTTTATTTGGTTGGGATCGCGTTGGGTTGGTTGTTAGGTT-- 344
QY 52 AspProArgArgAla 56
Db 343 -----CCTCGGCGA 335
RESULT 32
US-09-962-832-255
; Sequence 256, Application US/09962832
; GENERAL INFORMATION:
; APPLICANT: Eulner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 683290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/335,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 256
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; OS-09-962-832-256
Alignment Scores:
Pred. No.: 7.6 Length: 942
Score: 67.50 Matches: 17
Percent Similarity: 61.11% Conservative: 5
Best Local Similarity: 47.22% Mismatches: 11
Query Match: 21.99% Indels: 3
DB:
QY 21 ArgArgLeuGluHisThrPheLeuArgArgAlaThrArgPheTrpAspProArgArg 39
Db 620 AGACATCTGCTGATACCGCTACTATTTGATGATGTTCCATGCCCTTGACGGGAGA 679
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-Cpg-3
FILE REFERENCE: E01/1227

```

RESULT 33
; Sequence 1338, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, René
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 1338-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1338
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICACION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006912
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1338

Alignment Scores:
Pred. No.: 8.68 Length: 1037
Score: 67.50 Matches: 17
Percent Similarity: 61.11% Conservative: 5
Best Local Similarity: 47.22% Mismatches: 11
Query Match: 21.99% Indels: 3
DB: 16 Gaps: 2

Alignment Scores:
Pred. No.: 8.68 Length: 1037
Score: 67.50 Matches: 17
Percent Similarity: 61.11% Conservative: 5
Best Local Similarity: 47.22% Mismatches: 11
Query Match: 21.99% Indels: 3
DB: 15 Gaps: 2

US-10-031-158-14 (1-58) x US-10-172-118-1338 (1-1037)

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuMetLeuLeu---Arg 39
Db 620 AGACATCTGTGCTGCATACCGTACTATATTGATGATGATGTTTCAGGCCCTTGACGGAGA 679

TITLE OF INVENTION: CDNA EXPRESSED IN ADIPOCYTE DIFFERENTIATION
FILE REFERENCE: PA_0033_1S
CURRENT APPLICATION NUMBER: US/09/918,624B
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: 60/222,470
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 71
SOBQ ID NO 4
LENGTH: 2532
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: misc feature
NAME KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030113720A1 481536.3
US-09-918-624B-4

Alignment Scores:
Pred. No.: 29.8 Length: 2532
Score: 67.50 Matches: 17
Percent Similarity: 61.11% Conservative: 5
Best Local Similarity: 47.22% Mismatches: 11
Query Match: 21.99% Indels: 3
DB: 10 Gaps: 2

US-10-031-158-14 (1-58) x US-09-918-624B-4 (1-2532)

QY 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnPheSerLeuMetLeuLeu---Arg 39
Db 732 AGACATCTGTGCTGCATACCGTACTATATTGATGATGATGTTTCAGGCCCTTGACGGAGA 791

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/238,918
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
US-09-918-624B-4
LENGTH: 1037
TYPE: DNA
ORGANISM: Homo sapiens
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: 700-007-808A1
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.

```

```

FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SEQ ID NO: 7020
; LENGTH: 11838
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-891-7020

Alignment Scores:
Pred. No.: 251 Length: 11838
Score: 67.50 Matches: 17
Percent Similarity: 61.11% Conservative: 5
Best Local Similarity: 47.22% Mismatches: 11
Query Match: 21.99% Indels: 3
Db: 10 Gaps: 2

US-10-031-158-14 (1-58) x US-09-764-891-7020 (1-11838)
Qy 21 ArgArgLeuGluHisThrPheValPheLeuArgAsnSerLeuMetLeuIeu--Arg 39
Db 10840 AGACATCGCTGATACGCCACTATAATGATGATGTTTCCATGCCCTTGAGGAGA 10899
Qy 40 TyrIleGlyLysSargArgAlaThrArgPheTrpAspProArgArg 55
Db 10900 TAGTAGGAAAGAAAGAGG-----CAGTACTGGCCATGAGAAA 10941

RESULT 37
US-10-311-455-1165
; Sequence 1165, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; TITLE OF INVENTION: diagnosis of Diseases Associated with the Immune System by Determ
; FILE REFERENCE: 5013-1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO: 1165
; LENGTH: 13814
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: 4518
; OTHER INFORMATION: n is a or g or c or t
; US-10-311-455-1165

Alignment Scores:
Pred. No.: 311 Length: 13814
Score: 67.50 Matches: 18
Percent Similarity: 55.56% Conservative: 7
Best Local Similarity: 40.00% Mismatches: 15
Query Match: 21.99% Indels: 5
Db: 15 Gaps: 2

US-10-031-158-14 (1-58) x US-10-311-455-1165 (1-13814)

Qy 12 PhleuGinLeuLeuLeuLysGlnSerSerArgArgLeuGluHisThrPheValPheLeuArg 31

```

```

; Sequence 4936, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 4936
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE: OTHER INFORMATION: Clone ID: MRT4577_104499C.1
; US-10-425-115-4936

Alignment Scores:
Pred. No.: 1.98 Length: 314
Score: 67.00 Matches: 20
Percent Similarity: 45.76% Conservative: 7
Best Local Similarity: 33.90% Mismatches: 20
Query Match: 21.82% Indels: 12
Db: 18 Gaps: 3

US-10-031-158-14 (1-58) x US-10-425-115-4936 (1-314)
Qy 5 ProProSerProLeuPhePhePheIeuGln-----IeuLeuLysGlnSerSerArg 21
Db 311 CCCACCCCCCAGGT-----CATGCCCAATGCCTTTGGGTTTSCCAA 252
Qy 22 ArgLeuGluHisThrPheValPheLeuArgAsn----PheserLeuMetLeuLeuArg 39
Db 251 AGCTTCCCCTCAATCTTTAGGGCCACCTTGTGTCCT----- 198
Qy 40 TyrIleGlyLysSargArgAlaThrArgPheTrpAspProArgArgGlyThrPro 58
Db 197 -----AcACCCCCCAGGAACCTCTTCCCAGGAAATGCC 156

RESULT 39
US-10-027-632-252580/c
; Sequence 252580, Application US/10027632
; Publication No. US2002019837A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29

```

Page 16

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using sw model
 Run on: December 13, 2005, 08:18:33 ; Search time 181 Seconds
 Sequence: 1 MQMFPSPSPFLQLKQSS.....RYIGKRRATRFMDPQRGTP 58
 (without alignments)
 14.0-.795 Million cell updates/sec

Title: US-10-031-158B-14
 Perfect score: 58
 Scoring table: Oligo
 Searched: Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 408321

Minimum DB seq length: 8

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:
 1: geneseqp1980s:
 2: geneseqp1990s:
 3: geneseqp2000s:
 4: geneseqp2001s:
 5: geneseqp2002s:
 6: geneseqp2003s:
 7: geneseqp2003s:
 8: geneseqp2004s:
 9: geneseqp2005s:
 pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	9	15.5	9	ADW44402 Human TAR
2	9	15.5	9	ADW44401 Human TAR
3	9	15.5	9	ADW44406 Human TAR
4	8	13.8	8	ADW44405 Human TAR
5	8	13.8	9	ADW44404 Human TAR
6	10.3	9	ADH89809 Cell pene	
7	6	10.3	9	ADW44403 Human TAR
8	5	8.6	8	ABO06282 PROK1-1
9	5	8.6	8	Aek1508 GAG-bind
10	5	8.6	9	AAR59128 Peptide f
11	5	8.6	9	Aar38039 Hepatitis
12	5	8.6	9	Aay38106 Hepatitis
13	5	8.6	9	Aaw44612 Anti-fung
14	5	8.6	9	Aaw44677 Bacteric
15	5	8.6	9	ARY45508 Immunogen
16	5	8.6	9	Aay45674 Immunogen
17	5	8.6	9	Aay6768 Peptide f
18	5	8.6	9	Aay00589 Antifunga
19	5	8.6	9	Aab05513 Anti-fung
20	5	8.6	9	Aau00796 HIV-1 Tat
21	5	8.6	9	Abb08361 Synthetic
22	5	8.6	9	Aao15791 Human imm
23	5	8.6	9	Abp54737 HIV-1 tat
24	5	8.6	9	Abp54737 HIV-1 tat
25	5	8.6	9	ABR82213 Human ant
26	5	8.6	9	Aok65211 Human PIG
27	5	8.6	9	Ade97590 Immunogen
28	5	8.6	9	Adh8910 Cel1 pene
29	5	8.6	9	Adh44385 INI4a imm
30	5	8.6	9	Adh44376 INT4a imm
31	5	8.6	9	ADK84035 Human 191
32	5	8.6	9	ADK84519 Human 191
33	5	8.6	9	ADK85026 Human 191
34	5	8.6	9	ADK85074 Human 191
35	5	8.6	9	ADK87550 Human 191
36	5	8.6	9	Adk88447 Human 191
37	5	8.6	9	ADK83950 Human 191
38	5	8.6	9	ADK88445 Human 191
39	5	8.6	9	ADK84560 Human 191
40	5	8.6	9	ADK85620 Human 191
41	5	8.6	9	ADK84518 Human 191
42	5	8.6	9	ADK86036 Human 191
43	5	8.6	9	ADK86641 Human 191
44	5	8.6	9	ADK87058 Human 191
45	5	8.6	9	ADK87549 Human 191

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	9	9	ADW44402	Human TAR
2	9	15.5	ADW44401	Human TAR
3	9	15.5	ADW44406	Human TAR
4	8	13.8	ADW44405	Human TAR
5	8	13.8	ADW44404	Human TAR
6	10.3	9	ADH89809	Cell pene
7	6	10.3	9	ADW44403
8	5	8.6	8	ABO06282 PROK1-1
9	5	8.6	8	Aek1508 GAG-bind
10	5	8.6	9	AAR59128 Peptide f
11	5	8.6	9	Aar38039 Hepatitis
12	5	8.6	9	Aay38106 Hepatitis
13	5	8.6	9	Aaw44612 Anti-fung
14	5	8.6	9	Aaw44677 Bacteric
15	5	8.6	9	ARY45508 Immunogen
16	5	8.6	9	Aay45674 Immunogen
17	5	8.6	9	Aay6768 Peptide f
18	5	8.6	9	Aay00589 Antifunga
19	5	8.6	9	Aab05513 Anti-fung
20	5	8.6	9	Aau00796 HIV-1 Tat
21	5	8.6	9	Abb08361 Synthetic
22	5	8.6	9	Aao15791 Human imm
23	5	8.6	9	Abp54737 HIV-1 tat
24	5	8.6	9	Abp54737 HIV-1 tat
25	5	8.6	9	ABR82213 Human ant
26	5	8.6	9	Aok65211 Human PIG
27	5	8.6	9	Ade97590 Immunogen
28	5	8.6	9	Adh8910 Cel1 pene
29	5	8.6	9	Adh44385 INI4a imm
30	5	8.6	9	Adh44376 INT4a imm
31	5	8.6	9	ADK84035 Human 191
32	5	8.6	9	ADK84519 Human 191
33	5	8.6	9	ADK85026 Human 191
34	5	8.6	9	ADK85074 Human 191
35	5	8.6	9	ADK87550 Human 191
36	5	8.6	9	Adk88447 Human 191
37	5	8.6	9	ADK83950 Human 191
38	5	8.6	9	ADK88445 Human 191
39	5	8.6	9	ADK84560 Human 191
40	5	8.6	9	ADK85620 Human 191
41	5	8.6	9	ADK84518 Human 191
42	5	8.6	9	ADK86036 Human 191
43	5	8.6	9	ADK86641 Human 191
44	5	8.6	9	ADK87058 Human 191
45	5	8.6	9	ADK87549 Human 191

RESULT 1
 ADW44402 standard; peptide; 9 AA.
 ID ADW44402;
 AC XX
 DT 24-MAR-2005 (first entry)
 DE Human TARP polypeptide epitope TARP-27-35.
 KW T-cell receptor gamma alternate reading frame protein; TARP; immunogenicity; breast tumor; prostate tumor; cytostatic; neoplasm; receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2005000889-A1.
 PD 06-JAN-2005.
 XX
 PP 02-JUN-2004; 2004WO-US017574.
 PR 05-JUN-2003; 2003US-0476467P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Berzofsky JA, On S, Pastan I;
 XX
 DR WPI; 2005-091494/10.
 XX
 New T-cell receptor gamma alternate reading frame protein (TARP) polypeptide, useful for treating a subject having breast or prostate cancer and for generating an immune response to TARP-expressing breast and prostate cancer cells.
 XX
 Claim 2; SEQ ID NO 4; 83pp; English.
 XX
 The invention relates to an immunogenic T-cell receptor gamma alternate reading frame protein (TARP) polypeptide and the polynucleotide encoding it. The invention also relates to a vector comprising the TARP polynucleotide, a host cell transformed with the vector, a pharmaceutical composition comprising a therapeutic amount of the polypeptide or the polynucleotide in a pharmaceutical carrier, eliciting an immune response in a subject, inhibiting the growth of a breast cancer or a prostate cancer cell, a reagent comprising a tetramer of the polypeptide bound to HLA-A2 and streptavidin, where the reagent is labeled or unlabeled, and detecting T cells expressing CD8 that specifically recognize the TARP

CC polypeptide in a subject. Eliciting an immune response in a subject
 CC comprises administering the polypeptide or polynucleotide, thus producing
 CC an immune response in the subject. The immune response comprises a T cell
 CC response or inducing cytotoxic T cells that induce lysis of cells
 CC expressing the TARP polypeptide. The subject has breast cancer or
 CC prostate cancer. The immune response decreases the growth of the prostate
 CC cancer or breast cancer. The method further comprises administering an
 CC adjuvant to the subject. Inhibiting the growth of a breast cancer or
 CC prostate cancer cell comprises culturing cytotoxic T Lymphocytes (CTLs)
 CC or CTL precursor cells with the polypeptide and an antigen presenting
 CC cell to produce activated CTLs matured from the CTL precursors that
 CC recognize the breast cancer or the prostate cancer cells, and contacting
 CC the breast cancer or the prostate cancer cell with the activated CTLs or
 CC CTLs matured from the CTL precursors, thus inhibiting the growth of the
 CC breast cancer or the prostate cancer cell. The TARP polypeptide and
 CC polynucleotide are useful for treating a subject having breast or
 CC prostate cancer. The polypeptide is useful for generating an immune
 CC response to breast cancer and prostate cancer cells that express TARP
 CC polypeptides. This sequence represents a human TARP polypeptide epitope
 CC used in the scope of the invention.

SQ Sequence 9 AA;

Query Match 15.5%; Score 9; DB 9; Length 9;
 Best local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 27 FVFLRNFSL 35

Db 1 FVFLRNFSL 9

RESULT 2

ID ADW44401
 ID ADW44401 standard; peptide; 9 AA.

AC ADW44401;

XX DT 24-MAR-2005 (first entry)

DE Human TARP polypeptide epitope TARP-29-37.

KW T-cell receptor gamma alternate reading frame protein; TARP; neoplasm;

KW receptor.

OS Homo sapiens.

XX PN WO2005000889-A1.

XX PD 06-JAN-2005.

PP 02-JUN-2004; 2004WO-US017574.

XX PR 05-JUN-2003; 2003US-0476467P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Berzofsky JA, Oh S, Pastan I;

XX DR WPI; 2005-091494/10.

XX PT New T-cell receptor gamma alternate reading frame protein (TARP) polypeptide, useful for treating a subject having breast or prostate cancer and for generating an immune response to TARP-expressing breast and prostate cancer cells.

XX PS Claim 2; SEQ ID NO 3; 83pp; English.

The invention relates to an immunogenic T-cell receptor gamma alternate reading frame protein (TARP) polypeptide, useful for treating a subject having breast or prostate cancer and for generating an immune response to TARP-expressing breast and prostate cancer cells. The invention also relates to a vector comprising the TARP polynucleotide, a host cell transformed with the vector, a pharmaceutical

CC composition comprising a therapeutic amount of the polypeptide or the
 CC polynucleotide in a pharmaceutical carrier, eliciting an immune response
 CC in a subject, inhibiting the growth of a breast cancer or a prostate
 CC cancer cell, a reagent comprising a tetramer of the polypeptide bound to
 CC HLA-A2 and streptavidin, where the reagent is labeled or unlabeled, and
 CC detecting T cells expressing CD8 that specifically recognize the TARP
 CC polypeptide in a subject. Eliciting an immune response in a subject
 CC comprises administering the polypeptide or polynucleotide, thus producing
 CC an immune response in the subject. The immune response comprises a T cell
 CC response or inducing cytotoxic T cells that induce lysis of cells
 CC expressing the TARP polypeptide. The subject has breast cancer or
 CC prostate cancer. The immune response decreases the growth of the prostate
 CC cancer or breast cancer. The method further comprises administering an
 CC adjuvant to the subject. Inhibiting the growth of a breast cancer or
 CC prostate cancer cell comprises culturing cytotoxic T Lymphocytes (CTLs)
 CC or CTL precursor cells with the polypeptide and an antigen presenting
 CC cell to produce activated CTLs matured from the CTL precursors that
 CC recognize the breast cancer or the prostate cancer cells, and contacting
 CC the breast cancer or the prostate cancer cell with the activated CTLs or
 CC CTLs matured from the CTL precursors, thus inhibiting the growth of the
 CC breast cancer or the prostate cancer cell. The TARP polypeptide and
 CC polynucleotide are useful for treating a subject having breast or
 CC prostate cancer. The polypeptide is useful for generating an immune
 CC response to breast cancer and prostate cancer cells that express TARP
 CC polypeptides. This sequence represents a human TARP polypeptide epitope
 CC used in the scope of the invention.

SQ Sequence 9 AA;

Query Match 15.5%; Score 9; DB 9; Length 9;
 Best local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 29 FLRNFSML 37

ID ADW44406
 ID ADW44406 standard; peptide; 9 AA.

AC ADW44406;

XX DT 24-MAR-2005 (first entry)

DE Human TARP polypeptide epitope TARP-22-30.

KW T-cell receptor gamma alternate reading frame protein; TARP; neoplasm;

KW receptor.

OS Homo sapiens.

XX PN WO2005000889-A1.

XX PD 06-JAN-2005.

PP 02-JUN-2004; 2004WO-US017574.

XX PR 05-JUN-2003; 2003US-0476467P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Berzofsky JA, Oh S, Pastan I;

XX DR WPI; 2005-091494/10.

New T-cell receptor gamma alternate reading frame protein (TARP) polypeptide, useful for treating a subject having breast or prostate cancer and for generating an immune response to TARP-expressing breast and prostate cancer cells.

PS Example 2; SEQ ID NO 8; 83pp; English.

XX
XX The invention relates to an immunogenic T-cell receptor gamma alternate reading frame protein (TARP) polypeptide and the polynucleotide encoding it. The invention also relates to a vector comprising the TARP polynucleotide, a host cell transformed with the vector, a pharmaceutical composition comprising a therapeutic amount of the polypeptide or the polynucleotide in a pharmaceutical carrier, eliciting an immune response in a subject, inhibiting the growth of a breast cancer or a prostate cancer cell, a reagent comprising a tetramer of the polypeptide bound to HLA-A2 and streptavidin, where the reagent is labeled or unlabeled, and detecting T cells expressing CD8 that specifically recognize the TARP polypeptide in a subject. Eliciting an immune response in a subject comprises administering the polypeptide or polynucleotide, thus producing an immune response in the subject. The immune response comprises a T cell response or inducing cytotoxic T cells that induce lysis of cells expressing the TARP polypeptide. The subject has breast cancer or prostate cancer. The immune response decreases the growth of the prostate cancer or breast cancer. The method further comprises administering an adjuvant to the subject. Inhibiting the growth of a breast cancer or prostate cancer cell comprises culturing cytotoxic T lymphocytes (CTLs) or CTL precursor cells with the polypeptide and an antigen presenting cell to produce activated CTLs matured from the CTL precursors that recognize the breast cancer or the prostate cancer cells, and contacting the breast cancer or the prostate cancer cell with the activated CTLs or CTLs matured from the CTL precursors, thus inhibiting the growth of the breast cancer or the prostate cancer cell. The TARP polypeptide and polynucleotide are useful for treating a subject having breast or prostate cancer. The polypeptide is useful for generating an immune response to breast cancer and prostate cancer cells that express TARP polypeptides. This sequence represents a human TARP polypeptide epitope used in the scope of the invention.

SQ Sequence 9 AA;

Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 RLEHTFVFL 30

Db 1 RLEHTFVFL 9

RESULT 4
ID ADW44405 standard; peptide; 8 AA.

AC ADW44405;

XX 24-MAR-2005 (first entry)

DE Human TARP polypeptide epitope TARP-2-9.

XX KW T-cell receptor gamma alternate reading frame protein; TARP; KW immunogenicity; breast tumor; prostate tumor; cytostatic; neoplasm; KW receptor.

XX OS Homo sapiens.

XX PN WO200500889-A1.

XX XX 06-JAN-2005.

XX PF 02-JUN-2004; 2004WO-US017574.

XX PR 05-JUN-2003; 2003US-0476467P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Berzofsky JA, Oh S, Pastan I;

DR WPI; 2005-091494/10.

XX
XX New T-cell receptor gamma alternate reading frame protein (TARP) polypeptide, useful for treating a subject having breast or prostate cancer and for generating an immune response to TARP-expressing breast

XX
XX cancer cells.

PS Example 2; SEQ ID NO 7; 83pp; English.

XX
XX The invention relates to an immunogenic T-cell receptor gamma alternate reading frame protein (TARP) polypeptide and the polynucleotide encoding it. The invention also relates to a vector comprising the TARP polynucleotide, a host cell transformed with the vector, a pharmaceutical composition comprising a therapeutic amount of the polypeptide or the polynucleotide in a pharmaceutical carrier, eliciting an immune response in a subject, inhibiting the growth of a breast cancer or a prostate cancer cell, a reagent comprising a tetramer of the polypeptide bound to HLA-A2 and streptavidin, where the reagent is labeled or unlabeled, and detecting T cells expressing CD8 that specifically recognize the TARP polypeptide in a subject. Eliciting an immune response in a subject comprises administering the polypeptide or polynucleotide, thus producing an immune response in the subject. The immune response comprises a T cell or CTL precursor cells with the polypeptide and an antigen presenting cell to produce activated CTLs matured from the CTL precursors that recognize the breast cancer or the prostate cancer cells, and contacting the breast cancer or the prostate cancer cell with the activated CTLs or CTLs matured from the CTL precursors, thus inhibiting the growth of the breast cancer or the prostate cancer cell. The TARP polypeptide and polynucleotide are useful for treating a subject having breast or prostate cancer. The immune response decreases the growth of the prostate cancer or breast cancer. The method further comprises administering an adjuvant to the subject. Inhibiting the growth of a breast cancer or prostate cancer cell comprises culturing cytotoxic T lymphocytes (CTLs) or CTL precursor cells with the polypeptide and an antigen presenting cell to produce activated CTLs matured from the CTL precursors that recognize the breast cancer or the prostate cancer cells, and contacting the breast cancer or the prostate cancer cell with the activated CTLs or CTLs matured from the CTL precursors, thus inhibiting the growth of the breast cancer or the prostate cancer cell. The TARP polypeptide and polynucleotide are useful for generating an immune response to breast cancer and prostate cancer cells that express TARP polypeptides. This sequence represents a human TARP polypeptide epitope used in the scope of the invention.

SQ Sequence 8 AA;

Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 OMPPPSPL 8

Db 1 OMPPPSPL 8

RESULT 5
ID ADW44404

AC ADW44404 standard; peptide; 9 AA.

XX 24-MAR-2005 (first entry)

DE Human TARP polypeptide epitope TARP-29-37-9V.

XX KW T-cell receptor gamma alternate reading frame protein; TARP; KW immunogenicity; breast tumor; prostate tumor; cytostatic; neoplasm; KW receptor; mutein.

XX OS Homo sapiens.

XX PN WO200500889-A1.

XX PA Misc-difference 9 /note= "Wild-type Leu substituted by Val"

XX PN WO200500889-A1.

XX Key FH Location/Qualifiers

XX FT Misc-difference 9 /note= "Wild-type Leu substituted by Val"

PD 06-JAN-2005.

XX XX FF 02-JUN-2004; 2004WO-US017574.

XX XX PR 05-JUN-2003; 2003US-0476467P.

XX XX KW (USSH) US DEPT HEALTH & HUMAN SERVICES..

PA XX PT Berzofsky JA, Oh S, Pastan I;

XX DR WPI; 2005-091494/10.

XX XX PT New T-cell receptor gamma alternate reading frame protein (TARP) polypeptide, useful for treating a subject having breast or prostate cancer and for generating an immune response to TARP-expressing breast and prostate cancer cells.

XX PS Claim 2; SEQ ID NO 6; 83pp; English.

The invention relates to an immunogenic T-cell receptor gamma alternate reading frame protein (TARP) polypeptide and the polynucleotide encoding it. The invention also relates to a vector comprising the TARP polynucleotide, a host cell transformed with the vector, a pharmaceutical composition comprising a therapeutic amount of the polypeptide or the polynucleotide in a pharmaceutical carrier, eliciting an immune response in a subject, inhibiting the growth of a breast cancer or a prostate cancer cell, a reagent comprising a tetramer of the polypeptide bound to HLA-A2 and streptavidin, where the reagent is labeled or unlabeled, and detecting T cells expressing CD8 that specifically recognize the TARP polypeptide in a subject. Eliciting an immune response in a subject comprises administering the polypeptide or polynucleotide, thus producing an immune response in the subject. The immune response comprises a T cell expressing the TARP polypeptide. The subject has breast cancer or prostate cancer. The immune response decreases the growth of the prostate cancer or breast cancer. The method further comprises administering an adjuvant to the subject. Inhibiting the growth of a breast cancer or prostate cancer cell comprises culturing cytotoxic T lymphocytes (CTLs) or CTL precursor cells with the polypeptide and an antigen presenting cell to produce activated CTLs matured from the CTL precursors that recognize the breast cancer or the prostate cancer cells, and contacting the breast cancer or the prostate cancer cell with the activated CTLs or CTLs matured from the CTL precursors, thus inhibiting the growth of the breast cancer or the prostate cancer cell. The TARP polypeptide and polynucleotide are useful for treating a subject having breast or prostate cancer. The polypeptide is useful for generating an immune response to breast cancer and prostate cancer cell that express TARP polypeptides. This sequence represents a human TARP polypeptide epitope used in the scope of the invention.

XX SQ Sequence 9 AA;

Query Match 13.8%; Score 8; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

QY 29 PLRNFSIM 36

Db 1 PLRNFSIM 8

KW cardiotonic; cytostatic; tranquiliser; immunosuppressive; antidepressant;

KW anticonvulsant; antiinflammatory; analgesic; neuroleptic;

KW ophthalmological; antilulcer; cell-penetration; infectious disease;

KW diabetes type I; diabetes type II; Alzheimer's disease;

KW Parkinson's disease; cancer; prion disease; cardiovascular disease;

KW signal transduction.

XX OS Unidentified.

XX PN WO2003106491-A2.

XX PD 24-DEC-2003.

XX PR 18-JUN-2003; 2003WO-1B003163.

XX PR 18-JUN-2002; 2002SE-00001863.

XX PR 25-JUN-2002; 2002US-0391788P.

XX PA (CEPEP) CEPPEP AB.

Haelblirink M, Pooga M, Metsis M, Kogerman P, Valkna A, Meikas A; Lindgren M, Graaelund A, Eriksson G, Ostentsson CG, Budhina M; Zorko M, Elmquist A, Soomets U, Lundberg P, Jaervier P, Saar K; El-Andaloussi S, Kilk K, Dangel U;

XX DR WPI; 2004-090832/09.

XX Predicting, designing, detecting, and/or verifying novel cell-penetrating peptide based on assessment of bulk property value of sequences of cell-penetrating peptide.

XX PS Disclosure; Page 31; 148pp; English.

This invention relates to a novel method of identifying, designing, detecting, and/or verifying novel cell-penetrating peptide (CPP) based on assessment of bulk property value Z-E of sequences of CPP comprising 5 or more individual average interval values Z-B1, Z-E2, Z-E3, Z-E4 and Z-E5, where Z-B1, Z-E2, Z-E3, Z-E4 and Z-E5 are average values of the respective descriptor values for the residues in the amino acid sequence.

The invention may be useful for the development of compounds with an anti-diabetic, neuroprotective, nootropic, anti-parkinsonian, cardiotonic, cytostatic, tranquiliser, immunosuppressive, antidepressant, anticonvulsant, antiinflammatory, analgesic, neuroleptic, ophthalmological or antiulcer activity as a stimulator of cell-penetration. The method of the invention is useful for identifying a cell-penetrating peptide or protein and/or a cell-penetrating fragment of a peptide or protein. In addition, the invention may be useful for checking cellular penetration properties of a peptide, for producing a cell-penetrating and functional protein-mimicking peptide and for de novo design and production of an artificial cell-penetrating and/or and artificial cell-penetrating and functional protein-mimicking peptide. Compositions developed within the scope of the present invention may be useful for treating infectious diseases, diabetes type I, diabetes type II, Alzheimer's disease, Parkinson's disease, cancer, prion disease, cardiovascular disease or disorders resulting from perturbed signal transduction. The method of the invention is fast, efficient and reliable for identifying, detecting, designing CPPs and for screening cellular uptake of a broad variety of CPPs in vitro and in vivo. The present sequence is that of a peptide which is related to the invention.

XX SQ Sequence 9 AA;

Query Match 10.3%; Score 6; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 6; Conservative 0; Indels 0; Gaps 0;

QY 12 FLQLIK 17

Db 4 FLQLIK 9

RESULT 7

ADW44403

RESULT 6

ADH8809

ID ADH9809 standard; peptide; 9 AA.

AC ADH8809;

XX DT 22-APR-2004 (first entry)

DE Cell penetrating peptide (CPP) identification method-related peptide 111.

XX cell-penetrating peptide; CPP; bulk property value Z-E; Z-E1; Z-E2; Z-E3; Z-E4; Z-E5; antidiabetic; neuroprotective; nootropic; antiparkinsonian;

KW

ID	ADM44403	standard; peptide; 9 AA.	Query Match	10.3%	Score	6	DB	9	Length	9;
XX			Best Local Similarity	100.0%	Pred. No.	2e+06				
AC	ADM44403;		Matches	6	Conservative	0	Mismatches	0	Indels	0
XX			Ov	32	NFSIML	37				
DT	24-MAR-2005	(first entry)	Db	4	NFSIML	9				
XX										
DE	Human TARP polypeptide epitope	TARP-29-37-3A.	RESULT	8						
XX	T-cell receptor gamma alternate reading frame protein; TARP;		AB06282							
KW	immunogenicity; breast tumor; prostate tumor; cytostatic; neoplasm;		ID	AB06282	standard; peptide	8 AA.				
XX	receptor; mutein.		AC							
OS	Homo sapiens.		XX							
XX	Synthetic.		AAB06282;							
FH			XX							
FT	Key-difference	location/Qualifiers	03-OCT-2000	(first entry)						
FT	3	/note= "Wild-type Arg substituted by Ala"	XX							
PN	WO2005000889-A1.		DE	proSKI-1 putative zymogen cleavage site.						
XX			XX							
PD	06-JAN-2005.		XX	Human; pro-brain-derived neurotrophic factor; PROBDNF;						
XX			XX	subtilisin-kexin isoenzyme 1; SKI-1; proSKI-1 zymogen processing;						
PP	02-JUN-2004; 2004WO-US017574.		XX	antiliademic; cytostatic; vasotropin; SKI-1 inhibitor;						
PR	05-JUN-2003; 2003US-0476467P.		XX	hypercholesterolemia; liver steatosis; Ras-dependent cancer; restenosis;						
XX			XX	amyloid protein formation.						
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		XX							
XX			OS	Homo sapiens.						
PI	Berzofsky JA, Oh S, Pastan I;		OS	Mus sp.						
XX			XX	Rattus sp.						
DR			Key							
XX			Cleavage-site	4..5	Location/Qualifiers					
PT	New T-cell receptor gamma alternate reading frame protein (TARP)		XX							
PT	polypeptide, useful for treating a subject having breast or prostate		PN							
PT	cancer and for generating an immune response to TARP-expressing breast		XX							
PT	and prostate cancer cells.		PD							
XX			XX							
PS	Claim 2; SEQ ID NO 5; 83pp; English.		PF							
XX			XX							
CC	The invention relates to an immunogenic T-cell receptor gamma alternate		XX							
CC	reading frame protein (TARP) polypeptide and the polynucleotide encoding		XX							
CC	it. The invention also relates to a vector comprising the TARP		XX							
CC	polynucleotide, a host cell transformed with the vector, a pharmaceutical		XX							
CC	composition comprising a therapeutic amount of the polypeptide or the		XX							
CC	polynucleotide in a pharmaceutical carrier, eliciting an immune response		XX							
CC	in a subject, inhibiting the growth of a breast cancer or a prostate		XX							
CC	cancer cell, a reagent comprising a tetramer of the polypeptide bound to		XX							
CC	detecting T cells expressing C8 that specifically recognize the TARP		XX							
CC	polypeptide in a subject. Eliciting an immune response in a subject		XX							
CC	comprises administering the polypeptide or polynucleotide, thus producing		XX							
CC	an immune response in the subject. The immune response comprises a T cell		XX							
CC	response or inducing cytotoxic T cells that induce lysis of cells		XX							
CC	expressing the TARP polypeptide. The subject has breast cancer or		XX							
CC	prostate cancer. The immune response decreases the growth of the prostate		XX							
CC	cancer or breast cancer. The method further comprises administering an		XX							
CC	adjuvant to the subject. Inhibiting the growth of a breast cancer or		XX							
CC	prostate cancer cell comprises culturing cytotoxic T lymphocytes (CTLs)		XX							
CC	or CTL precursor cells with the polypeptide and an antigen presenting		XX							
CC	cell to produce activated CTLs matured from the CTL precursors that		XX							
CC	recognize the breast cancer or the prostate cancer cells, and contacting		XX							
CC	the breast cancer or the prostate cancer cell with the activated CTLs or		XX							
CC	CTLs matured from the CTL precursors, thus inhibiting the growth of the		XX							
CC	breast cancer or the prostate cancer cell. The TARP polypeptide and		XX							
CC	polynucleotide are useful for treating a subject having breast or		XX							
CC	prostate cancer. The polypeptide is useful for generating an immune		XX							
CC	response to breast cancer and prostate cancer cell that express TARP		XX							
CC	used in the scope of the invention.		XX							
SQ	Sequence 9 AA:		SQ	Sequence 8 AA;						
	Query Match	8.6%	Score	5	DB	3	Length	8		
	Best Local Similarity	100.0%	Pred. No.	2e+06						
	Matches	5	Conservative	0	Mismatches	0	Indels	0	Gaps	0

Db	5	SLMLL 9	DB Hepatitis B virus-derived HLA-binding peptide.
XX			XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC;
RESULT 11			KW major histocompatibility complex; viral infection; anticancer;
ID AAY38039			KW prostate cancer; Lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
XX			XX Hepatitis B virus.
AC AAY38039;			XX
XX			PN WO9403205-A1.
DT 29-SEP-1999	(first entry)		PD 17-FEB-1994.
XX			XX
DE Hepatitis B virus-derived HLA-binding peptide.			PR 06-AUG-1993; 93WO-US007421.
XX			XX
KW Immunoigen; HLA; human leukocyte antigen; binding motif; antiviral; MHC;			PR 07-AUG-1992; 92US-00926666.
KW major histocompatibility complex; viral infection; anticancer;			PR 05-MAR-1993; 93US-00027746.
KW prostate cancer; Lymphoma; hepatitis; AIDS; diagnostic; diagnosis.			PA (CYTE-) CYTEL CORP.
OS Hepatitis B virus.			XX
XX			PT Kubo RT, Grey HM, Sette A, Celis E;
PN WO9403205-A1.			XX
XX			DR DR
PD 17-FEB-1994.			XX
XX			PT Peptide which specifically binds selected MHC allele - used to induce an
PF 06-AUG-1993; 93WO-US007421.			PT immune response for treatment or prevention of viral infection or cancer,
XX			PT or for diagnosis.
PR 07-AUG-1992; 92US-00926666.			XX
PR 05-MAR-1993; 93US-00027746.			PS Disclosure; Page 107; 150pp; English.
XX			XX
PA (CYTE-) CYTEL CORP.			CC The sequence is a specific example of a group of new immunogenic peptides
XX			CC having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For
PT Kubo RT, Grey HM, Sette A, Celis E;			CC example, the peptides having an HLA-A3.2 binding motif each have 9-10
XX			CC residues and contain, from the N-terminus to the C-terminus, (a) a first
DR WPI; 1994-065403/08.			CC conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and
XX			CC (b) a second conserved residue of K, R, Y, H or F, where the first and
PT Peptide which specifically binds selected MHC allele - used to induce an			CC second conserved residues are separated by 6-7 residues. The peptides are
PT immune response for treatment or prevention of viral infection or cancer,			CC capable of binding selected MHC molecules and inducing an immune
PT or for diagnosis.			CC response. They can be used to treat and/or prevent viral infection and
XX			CC cancer e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also
PS Disclosure; Page 106; 150pp; English.			CC be used to produce antibodies for use as diagnostic or therapeutic
XX			CC agents. The peptides can also be used as diagnostic agents.
CC The sequence is a specific example of a group of new immunogenic peptides			XX
CC having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For			SQ Sequence 9 AA;
CC example, the peptides having an HLA-A3.2 binding motif each have 9-10			Query Match 8.6%; Score 5; DB 2; Length 9;
CC residues and contain, from the N-terminus to the C-terminus, (a) a first			Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
CC conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and			Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC (b) a second conserved residue of K, R, Y, H or F, where the first and			QY 34 SLMLL 38
CC second conserved residues are separated by 6-7 residues. The peptides are			Db 3 SLMLL 7
CC capable of binding selected MHC molecules and inducing an immune			
CC response. They can be used to treat and/or prevent viral infection and			
CC cancer e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also			
CC be used to produce antibodies for use as diagnostic or therapeutic			
CC agents. The peptides can also be used as diagnostic agents			
XX			
SQ Sequence 9 AA;			RESULT 13
Query Match 8.6%; Score 5; DB 2; Length 9;			AAW44612
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;			ID AAW44612 standard; peptide; 9 AA.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			XX
QY 34 SLMLL 38			AC AAW44612;
Db 3 SLMLL 7			XX
RESULT 12			DT 27-APR-1998 (first entry)
AAV38105			XX
ID AAV38106 standard; Peptide; 9 AA.			DE Anti-fungal peptide #213 based on BPI protein (residues 142-169).
XX			XX
AC AAV38106;			KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
XX			KW polymorphonuclear leukocyte; fungicide.
DT 29-SEP-1999 (first entry)			XX
XX			OS Synthetic.
OS Mammalia.			XX
FR Modified-site 9	Location/Qualifiers		FT /note= "C-terminal amide"
FT			

XX WO9704008-A1.
 XX PD 06-FEB-1997.
 XX PT Recombinant production of bactericidal/permeability increasing protein by expression as a fusion protein in microbial host cells, then cleaving
 PT the BPI peptide from the carrier.
 PT XX
 XX PR 21-MAR-1996; 96WO-US003845.
 XX PR 20-JUL-1995; 95US-00504841.
 XX PS Claim 10; Page 136; 186pp; English.
 XX CC A new recombinant DNA vector construct has been developed which encodes a
 CC fusion protein and is suitable for introduction into a bacterial host.
 CC The vector comprises: (a) DNA encoding at least one cationic
 CC bactericidal/permeability increasing peptide (BPI); (b) DNA encoding a
 CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 CC located between (a) and (b). The present sequence represents a
 CC specifically claimed BPI peptide. The peptides have many uses including
 CC the treatment of bacterial and fungal infections. BPI peptides also bind
 CC to endotoxins and heparin, neutralising their effects. The peptides have
 CC further been shown to inhibit angiogenesis (partly due to heparin-binding
 CC activity). The fusion proteins have been found to be expressed in large
 CC amounts without significant proteolysis, and in some cases are actually
 CC secreted from the host cells. This allows the indirect production of anti-
 CC -microbial BPI peptides in microbial hosts.
 XX SQ Sequence 9 AA:
 Query Match 8 6%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Mismatches 5; Conservative 0; Indels 0; Gaps 0;
 Matches 5; CC
 QY 13 LQLLK 17
 Db 4 LQLLK 8
 RESULT 14
 AAW43777
 ID AAW43777 standard; peptide; 9 AA.
 XX AC AAW43777;
 XX DT 20-APR-1998 (first entry)
 DB Bactericidal/permeability increasing peptide XMP-382.
 XX KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
 KW fungal infection; fungal infection; endotoxin; heparin; angiogenesis;
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Location/Qualifiers
 FT 9 /note= "Amidated"
 XX PN WO9735009-A1.
 XX PD 25-SEP-1997.
 XX PP 13-MAR-1998; 98WO-US005039.
 XX PR 13-MAR-1998; 98WO-US005039.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PT Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX DR WPI; 1999-551214/46.
 XX PT New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX PA Claim 1; Page 37; 150pp; English.
 XX PS
 XX CC AAY45390 to AY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known

as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A2.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans).⁹ prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above

xx

Sequence 9 AA;

Query Match 8.6%; Score 5; DB 2; length 9;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 34 S|MLL 38
Db 1 S|MLL 5

Search completed: December 13, 2005, 08:21:44
Job time : 183 secs

THIS PAGE BLANK (USPTO)

Copyright (c) 1993 - 2005 GenCore version 5.1.6 CompuGen Ltd.

OM protein - protein search, using SW model
Run on: December 13, 2005, 08:18:36 ; Search time 37 Seconds
Minimum DB seq length: 8
Maximum DB seq length: 10

Title: US-10-031-158B-14
Perfect score: 58
Sequence: 1 MQMFPSSPLFFFLQLQKQSS.....RYIGKRRATRFWDPRRGTP 58

Scoring table: OLIGO² Gapop=60.0 , Gapext: 60.0

Searched: 283416 seqs, 96216763 residues
Word size : 0

Total number of hits satisfying chosen parameters: 645
Minimum DB seq length: 8
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries
Database : PIR 80.0*

1: piri: *
2: pirz: *
3: pix3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4	6.9	8	PC4131 hypothetical protein 8 [imported] - <i>Pseudomonas aeruginosa</i> (fragment)
2	4	6.9	10	A56633 neomyosupressin -
3	4	6.9	10	A32543 cardioexcitatory n
4	3	5.2	2	A44950 neuropeptide Led-C
5	3	5.2	8	A611348 red pigment-concen
6	3	5.2	8	S08995 hypothetrical prote
7	3	5.2	8	A49823 neomyosuppressin -
8	3	5.2	8	A28004 adipokinetic hormo
9	3	5.2	8	A433976 adipokinetic hormo
10	3	5.2	8	A433976 hypothetrical prote
11	3	5.2	8	T10077 hypothetrical prote
12	3	5.2	8	S19288 acylase - Kluvera
13	3	5.2	8	S21288 lectin - potato (f
14	3	5.2	8	A05169 neuropeptide M-I -
15	3	5.2	8	J50316 leucokinin VI - Ma
16	3	5.2	8	S71919 alcohol dehydrogen
17	3	5.2	9	A61102 parathyroid hormon
18	3	5.2	9	A60410 Ig heavy chain CRD
19	3	5.2	10	S019297 orf AB protein - S
20	3	5.2	9	A31576 xylose isomerase (
21	3	5.2	9	PCT076 spectrin alpha cha
22	3	5.2	10	A60624 angiotensin I - ja
23	3	5.2	10	A60410 beta-neendorphin
24	3	5.2	10	S019297 hypertrehalosemic
25	3	5.2	10	A60421 hypertrehalosemic
26	3	5.2	10	S08998 hypertrehalosemic
27	3	5.2	10	A63381 hypertrehalosemic
28	3	5.2	10	JN0440 peptide-N-(N-acet
29	3	5.2	10	PQ0753 beta-fructofuranos

ALIGNMENTS

RESULT 1	QY	20	SRR1	23	Db	5	SRR1	8
A56633								
neomyosupressin - flesh fly (<i>Sarcophaga bullata</i>)								
N;Alternate names: Neb-MS								
C;Species: <i>Sarcophaga bullata</i>								
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004								
C;Accession: A56633								
R;Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; Buend, H.; De Loof, A.								
Comp. Biochem. Physiol. C 102, 239-245, 1992								
A;Title: Isolation, primary structure and synthesis of neomyosupressin, a myoinhibiting								
A;Reference number: A56633; PMID:9307886; PMID:135537								
A;Accession: A56633								
A;Molecule type: protein								
A;Residues: 1-10 <PON>								
A;Cross-references: UNIPROT:P61850; UNIPARC:UPI000003AD0A								
A;Experimental source: head								
A;Note: sequence extracted from NCBI backbone (NCBIPR:119072)								
C;Keywords: amidated carboxyl end; neuropeptide F;10;Modified site: amidated carboxyl end (Phe) #status experimental								

Query Match 6.9%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e-03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 VFRL 31
 Qy |||||
 Db 6 VFRL 9

RESULT 3

A22543
 cardioexcitatory neuropeptide - desert locust
 C;Species: *Schistocerca gregaria* (Desert locust)
 C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 05-Oct-2004
 C;Accession: A32543
 R;Robb, S.; Packman, L.C.; Evans, P.D.
 Biochem. Biophys. Res. Commun. 160, 850-856, 1989
 A;Title: Isolation, primary structure and bioactivity of SchistoFLRF-amide, a FMRF-amide
 A;Reference number: A32543; MUID:89246543; PMID:2719702
 A;Accession: A32543
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <ROB>
 A;Cross-references: UNIPROT:P38553; UNIPARC:UPI00003AD64
 A;Keywords: amidated carboxyl end; neuropeptide
 F;1/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 6.9%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Db 6 VFRL 9

RESULT 4

A44960
 neuropeptide Ied-CC-I - Colorado potato beetle (Colorado potato beetle)
 C;Species: *Lepinotarsa decemlineata* (Colorado potato beetle)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: A44960
 R;Graede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
 A;Reference number: A44960; MUID:90160053; PMID:2576128
 A;Accession: A44960
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 C;Cross-references: UNIPROT:P04548; UNIPARC:UPI000012CDBB
 C;Superfamily: adipokinetic hormone
 C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 5.2%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Db 6 VFRL 9

Qy 32 NFS 34
 Qy |||||
 Db 3 NFS 5

RESULT 5

A61348
 red pigment-concentrating hormone - northern shrimp
 N;Alternate names: blanching hormone
 C;Species: *Pandalus borealis* (northern shrimp)
 C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
 C;Accession: A61348; S07139
 R;Fernlund, P.; Jansson, L.
 Science 177, 173-175, 1972
 A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
 A;Reference number: A61348; MUID:72228738; PMID:5041363
 A;Accession: A61348
 A;Molecule type: protein

Query Match 5.2%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Db 3 NFS 5

RESULT 6

S08995
 hypertrehalosemic hormone I - oriental cockroach
 N;Alternate names: Pea-CAH-I
 C;Species: *Blatt orientalis* (oriental cockroach)
 C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C;Accession: S08995
 R;Graede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
 analia and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombard
 A;Reference number: S08995; MUID:90253659; PMID:2340112
 A;Accession: S08995
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Cross-references: UNIPROT:P04548; UNIPARC:UPI000012CDBB
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 5.2%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Db 3 NFS 5

RESULT 7

A49823
 adipokinetic hormone I - American cockroach
 N;Alternate names: periplaneta americana (American cockroach)
 C;Species: *Periplaneta americana* (American cockroach)
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C;Accession: A49823
 R;Scarborough, R.M.; Jamieson, G.C.; Kalish, P.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
 A;Reference number: A49823; MUID:84298179; PMID:6591205
 A;Accession: A49823
 A;Molecule type: protein
 A;Residues: 1-8 <SGA>
 A;Cross-references: UNIPROT:P04548; UNIPARC:UPI000012CDBB

C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 5.2%; Score 3; DB 2; Length 8;

Matches 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

QY 32 NFS 34

Db 3 NFS 5

RESULT 8

A28004 adipokinetic hormone G - two-spotted cricket

N;Alternate names: AKH-G

C;Species: Gryllus bimaculatus (two-spotted cricket)

C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C;Accession: A28004

R;Gaede, G.; Rinehart, K.L.

Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide

A;Reference number: A28004; MUID:88106553; PMID:3426616

A;Accession: A28004

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P14086; UNIPARC:UPI000012576P

A;Note: the amino-terminal residue forms pyrrolidine carboxylic acid; therefore, we have

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 5.2%; Score 3; DB 2; Length 8;

Matches 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

QY 32 NFS 34

Db 3 NFS 5

RESULT 9

A33976 hypertrehalosemic hormone - yellow mealworm

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004

C;Accession: A433976

R;Gaede, G.; Rosinski, G.

peptides 11, 455-459, 1990

A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetles

A;Reference number: A433976; MUID:90341081; PMID:2381871

A;Accession: A433976

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P25419; UNIPARC:UPI000012CDC8

C;Superfamily: C-superofamily

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: amidated carboxyl end (Trp) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 5.2%; Score 3; DB 2; Length 8;

Matches 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

QY 32 NFS 34

Db 3 NFS 5

RESULT 10

A;Status: preliminary

A;Molecule type: protein

A;Cross-references: UNIPROT:Q7M124; UNIPARC:UPI000017AA77

B33976 hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: B433976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from *Kl*
A;Reference number: S19288; MUID:92109664; PMID:1764029
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Cross-references: UNIPROT:Q7M124; UNIPARC:UPI000017AA77
Query Match Best Local Similarity 5.2%; Score 3; DB 2; Length 8;
Matches 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 41 IGK 43
 Db 6 IGK 8

RESULT 13
 S21288
 lectin - potato (fragment)
 C;Species: *Solanum tuberosum* (potato)
 C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C;Accession: S21288
 R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Siddebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A;Title: Chitin-binding proteins in potato (*Solanum tuberosum* L.) tuber. Characterization
 A;Reference number: S21288; PMID:92272683; PMID:1590771
 A;Accession: S21288
 A;Molecule type: protein
 A;Residues: 1-8 <WIL>
 A;Cross-references: UNIPROT:Q7M1V6; UNIPARC:UPI000017B0BF

A;Experimental source: var. Ulster Sceptre
 C;Function:
 A;Description: may be involved in defence mechanism of the plant
 C;Keywords: hydroxyproline; lectin

Query Match 5.2%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 QSS 20
 Db 1 QSS 3

A;Cross-references: UNIPROT:P19988; UNIPARC:UPI000012E29E
 C;Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
 F;1;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8;Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 5.2%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Search completed: December 13, 2005, 08:27:10
 Job time : 39 secs

Query Match 5.2%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 PSP 8
 Db 5 PSP 7

RESULT 14

A05169

neuropeptide M-I - American cockroach

C;Species: *Periplaneta americana* (American cockroach)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C;Accession: A05169

R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas

A;Reference number: A90118; MUID:85046530; PMID:6548628

A;Accession: A05169

A;Molecule type: protein

A;Residues: 1-8 <WIL>

A;Cross-references: UNIPROT:PO4548; UNIPARC:UPI000017BB15
 C;Keywords: neuropeptide

Query Match 5.2%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 NFS 34
 Db 3 NFS 5

RESULT 15

JS3116
 Leucokinin VI - Madeira cockroach

C;Species: *Leucophaea maderae* (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS3116

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987

A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic

A;Reference number: JS3115

A;Accession: JS3116

A;Molecule type: protein

A;Residues: 1-8 <HOL>

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model
 Run on: December 13, 2005, 08:18:33 ; Search time 226 Seconds
 Minimum DB seq length: 8 (without alignments)
 Maximum DB seq length: 10
 Post-processing: Listing first 45 summaries

Title: US-10-031-158B-14
 Perfect score: 58
 Sequence: 1 MQMFPSPSPLFFLQLIKQSS.....RYIGKRRATRFWDDPRRGTP 58

Scoring table: OLIGO

Searched: Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 2877

Minimum DB seq length: 8
 Maximum DB seq length: 10

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	6.9	8	2	015896_BABBO
2	4	6.9	9	2	088889_MOUSE
3	4	6.9	10	1	FARP_LCMI
4	4	6.9	10	1	FARP_SCHGR
5	4	6.9	10	1	LCMS_LEUMA
6	4	6.9	10	1	NEMS_SARBU
7	4	6.9	10	2	Q6A370_9FILI
8	4	6.9	10	2	Q76M18_9TMBL
9	3	5.2	8	1	AKHG_GRYBI
10	3	5.2	8	1	AKH_RONMI
11	3	5.2	8	1	CADI_ENTFA
12	3	5.2	8	1	FAR_PANRE
13	3	5.2	8	1	FAR_PENMO
14	3	5.2	8	1	FAR2_MACRS
15	3	5.2	8	1	FAR3_HOMAM
16	3	5.2	8	1	FAR4_HOMAM
17	3	5.2	8	1	HTF1_BLAOR
18	3	5.2	8	1	HTF1_LEPDE
19	3	5.2	8	1	HTF1_PERAM
20	3	5.2	8	1	HTF_TBMMO
21	3	5.2	8	1	HTF_ZOPRIO
22	3	5.2	8	1	LCK6_LEUMA
23	3	5.2	8	1	RPCH_PANBO
24	3	5.2	8	1	RPCH51_YRAST
25	3	5.2	8	2	P82858_BASII
26	3	5.2	8	2	Q69Y18_HUMAN
27	3	5.2	8	2	Q8TF07_HUMAN
28	3	5.2	8	2	Q7MD01_HUMAN
29	3	5.2	8	2	Q8BS89_STPBU
30	3	5.2	8	2	Q78544_BPR17
31	3	5.2	8	2	Q40530_TOBAC

ALIGNMENTS

32	3	5.2	8	2	Q6UJ68_SOYBN	Q6ic68_glycine_max
33	3	5.2	8	2	Q70Y84_9IAWI	Q70y84_plectranthus
34	3	5.2	8	2	Q7MV6_SCOLTU	Q7mv6_solanum_tub
35	3	5.2	8	2	Q9RER0_SHIDY	Q9550_shigella_dy
36	3	5.2	8	2	Q79163_SNNSP	Q7sf63_synechococc
37	3	5.2	8	2	Q7M124_KUICI	Q7m124_kluyvera_ci
38	3	5.2	8	2	Q78D6_KAT	Q78D6_rattus_norv
39	3	5.2	8	2	Q8RM9_MOUSE	Q835m9_mus_musculu
40	3	5.2	8	2	Q9ET16_MESAU	Q9at16_mesocricetus
41	3	5.2	8	2	Q9ET17_MOSCR	Q9et17_mus_caroli
42	3	5.2	8	2	Q9ET18_MUSSP	Q9et18_mus_spretus
43	3	5.2	8	2	Q6PUD7_SV40	Q6ud5_simian_viru
44	3	5.2	8	2	Q6PUD9_SV40	Q6ud9_simian_viru

{1}

{2}

{3}

{4}

{5}

{6}

{7}

{8}

{9}

{10}

{11}

{12}

{13}

{14}

{15}

{16}

{17}

{18}

{19}

{20}

{21}

{22}

{23}

{24}

{25}

{26}

{27}

{28}

{29}

{30}

{31}

{32}

{33}

{34}

{35}

{36}

{37}

{38}

{39}

{40}

{41}

{42}

{43}

{44}

{45}

{46}

{47}

{48}

{49}

{50}

{51}

{52}

RT "Provirus integration into a gene encoding a ubiquitin-conjugating enzyme results in a placental defect and embryonic lethality.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12412-12417(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SV;
 RX MEDLINE=9913641;
 RA Miller U., Grams A., Martinez-Noel G., Copeland N.G., Gilbert D.J., Jenkins N.A., Harbers K.;
 RT "Structure of the gene encoding the ubiquitin-conjugating enzyme UbcM, characterization of its promoter, and chromosomal location.";
 RL Gene 224:109-116 (1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SV;
 RA Mueller U., Grams A., Martinez-Noel G., Harbers K.;
 RL Muelle U., Grams A., Martinez-Noel G., Harbers K.;
 DR EMBL; AF071557; ADN010128; 1; -; Genomic DNA.
 FT MGI; MGI:1109240; UBE213.
 SQ NON TER 9 AA; 1063 MW; C90F97341415BDD CRC64;
 SEQUENCE 9 AA; 1063 MW; C90F97341415BDD CRC64;

Query Match 6.9%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 VFLR 31
 Db 6 VFLR 9

RESULT 3
 FARP-LOCM1 STANDARD; PRT; 10 AA.
 ID FARP-LOCM1 STANDARD; PRT; 10 AA.
 AC P84307; P38553;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-2005 (Rel. 46, Last annotation update)
 DE SchistofURFamide (PDVDFURF-amide) (Cardioexcitatory neuropeptide).
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Acriidae; Cyrtacanthacridinae; Schistocerca.
 OC NCBI_TaxID=7010;
 RN [1]
 RP PROTEIN SEQUENCE, AND FUNCTION.
 RC TISSUE=Thoracic nervous system.
 RX MEDLINE=8924543; PubMed=2219702;
 CC Robb S., Packman L.C., Evans P.D.;
 RT "Isolation, primary structure and bioactivity of schistofURF-amide, a PMRF-amide-like neuropeptide from the locust, Schistocerca gregaria,"
 RL Biochem. Biophys. Res. Commun. 160:850-856 (1989).
 CC -1- FUNCTION: Muscle inhibiting agent. Involved in the neural control
 of the visceral muscles of the heart, accessory glands and
 oviduct. May be involved in the regulation of saliva secretion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR PIR; A32243; A32243.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RBS 10 AA; 10 Phenylalanine amide.
 SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 6.9%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 VFLR 31
 Db 6 VFLR 9

RESULT 4
 FARP-SCHGR STANDARD; PRT; 10 AA.
 ID FARP-SCHGR STANDARD; PRT; 10 AA.
 AC P84307; P38553;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DE SchistofURFamide (PDVDFURF-amide) (Cardioexcitatory neuropeptide).
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 OC Acridoidea; Acriidae; Cyrtacanthacridinae; Schistocerca.
 OC NCBI_TaxID=7010;

PROTEIN SEQUENCE, AND FUNCTION.
 TISSUE=Thoracic nervous system.
 MEDLINE=8924543; PubMed=2219702;

CC Robb S., Packman L.C., Evans P.D.;
 RT "Isolation, primary structure and bioactivity of schistofURF-amide, a PMRF-amide-like neuropeptide from the locust, Schistocerca gregaria,"
 RL Biochem. Biophys. Res. Commun. 160:850-856 (1989).
 CC -1- FUNCTION: Muscle inhibiting agent. Involved in the neural control
 of the visceral muscles of the heart, accessory glands and
 oviduct. May be involved in the regulation of saliva secretion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

CC -----
 DR PIR; A32243; A32243.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RBS 10 AA; 10 Phenylalanine amide.
 SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 6.9%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 VFLR 31
 Db 6 VFLR 9

RESULT 5
 LCMS-DEUMA STANDARD; PRT; 10 AA.
 ID LCMS LEUMA; P21174; P41497;
 AC 01-MAY-1991 (Rel. 18, Created)
 DT 01-FEB-2004 (Rel. 47, Last annotation update)
 DT 05-JUL-2004 (Rel. 47, Last annotation update)
 DE Leucophphaea maderae (Madara cockroach);
 OS Leucophphaea maderae (Madara cockroach);
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophphaea.
 OC NCBI_TaxID=6988;

NCBI_TaxID=6988;

[1]

RT This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

CC Amidation; Direct protein sequencing; Neuropeptide.

FT MOD_RES 10 10 Phenylalanine amide.

[1]

RP PROTEIN SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M.; Cook B.J.; Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucomyosupressin, an
 insect neuropeptide that inhibits spontaneous contractions of the
 cockroach hindgut.";
 RT Comp. Biochem. Physiol. 85C:329-333(1986).
 CC -1- FUNCTION: Inhibits the spontaneous contractions of cockroach
 protodeum (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.

RESULT 7
 Q6A3T0_9FIL1 PRELIMINARY; PRT; 10 AA.
 ID Q6A3T0_9FIL1 PRELIMINARY;
 AC Q6A3T0;
 DT 25-OCT-2004 (TREMBrel; 28; Created)
 DT 25-OCT-2004 (TREMBrel; 28; Last sequence update)
 DT 25-OCT-2004 (TREMBrel; 28; Last annotation update)
 DE ATP synthase beta subunit (EC 3.6.3.14) (Fragment).
 GN Name=cpdB;
 OS Name=cpdB;
 OG Chloroplast
 OC Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Moniliomorphes; Filicophyt; Marattiopsida; Marattiaceae;
 OC Marattiaceae; Archangiopteris.
 OX NEBI_TAXID=203826;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Chiang T., Chiang Y., Chou C., Cheng Y., Chiou W.;
 RT "Phylogenetic analysis and conservation of Archangiopteris somai and A. itoi
 (Marattiaceae, Pteridophyta) based on nucleotide variation of cpDNA
 atpB-rbcL intergenic spacer.";
 RT Submitted (AUG-2004) to the EMBL/GenBank/DDJB databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RA Chiang Y.C.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDJB databases.
 DR EMBL; AU05259; CAD44048.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Chloroplast; Hydrolase.
 FT NON_TER
 SQ SEQUENCE 10 AA; 1195 MW; 982AF009C737645 CRC64;

Query Match 6.9%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 VFILR 9

RESULT 6
 NEMS_SARBU STANDARD; PRT; 10 AA.
 ID P61850; P41494; Q9VQ91;
 AC P61850; P41494; Q9VQ91; 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Neomyosupressin (Neb-MS) (TPDVHFLRFamide).
 GN Name=NEMS;
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata);
 OC Dikoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga; Neobellieria.
 OX NCBI_TaxID=7385;
 RN [1]

RP PROTEIN SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=93049886; PubMed=1358537;
 RA Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.;
 RT "Isolation, primary structure and synthesis of neomyosupressin, a
 myoinhibiting neuropeptide from the grey fleshfly, Neobellieria
 bullata.";
 RT Comp. Biochem. Physiol. 102C:239-245(1992).
 CC -1- FUNCTION: Myoinhibiting neuropeptide.
 CC -1- SUBCELLULAR LOCATION: Secreted.

This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

RESULT 8
 Q76ML8_9TELE
 ID Q76ML8_9TELE PRELIMINARY; PRT; 10 AA.
 AC Q76ML8;
 DT 05-JUL-2004 (TREMBrel; 27; Created)
 DT 05-JUL-2004 (TREMBrel; 27; Last sequence update)
 DT 01-FEB-2005 (TREMBrel; 29; Last annotation update)
 DE NADH dehydrogenase subunit 6 (Fragment).
 GN Name=Nb6;
 OS Eurypharynidae; Eurypharynx.
 OG Mitochondrion.
 OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
 scale gene rearrangements originated within the eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDJB databases.

Query Match 6.9%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 5.2%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	29	FIR	31
Db	5	FIR	7

RESULT 15
 FAR3_HOMAM STANDARD PRT: 8 AA.
 AC P41486;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE FMRFamide-like neuropeptide 3 (FIR 3) (F2).
 OS Homarus americanus (American lobster).
 OC Eukaryote; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Bivalvia; Decapoda; Plecoyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID=6706;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE:88116164; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT "Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: isolation and sequence
 analysis of two closely related peptides.";
 RL J. Comp. Neurol. 266:16-26 (1987).
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- MISCELLANEOUS: Pericardial organs release this peptide with 100 mm
 potassium in the presence of calcium.
 CC -- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC
 CC Amidation; Direct protein sequencing; Neuropeptide.
 KW Phenylalanine amide.
 FT MOD_RES 8 Ph
 PT SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;
 SQ
 Query Match 5.2%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	29	FIR	31
Db	5	FIR	7

Search completed: December 13, 2005, 08:25:36
 Job time : 228 Secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: December 13, 2005, 08:18:37 ; Search time 46 Seconds

Sequence: 1 MQMPPPSPLPFOLLKQSS.....RYIICKKRATRFWDPRRGTP 58

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Title: US-10-031-158B-14
Perfect score: 58
Sequence: 1 MQMPPPSPLPFOLLKQSS.....RYIICKKRATRFWDPRRGTP 58

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 62763

Minimum DB seq length: 8

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_5/ptodata/1/iaa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile81.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	8.6	9	1 US-08-621-803-221	Sequence 221, App
2	5	8.6	9	1 US-08-621-213	Sequence 213, App
3	5	8.6	9	2 US-08-159-339A-343	Sequence 343, App
4	5	8.6	9	2 US-08-159-339A-405	Sequence 405, App
5	5	8.6	9	2 US-09-217-352-221	Sequence 221, App
6	5	8.6	9	2 US-09-677-64B-213	Sequence 213, App
7	5	8.6	9	2 US-09-792-48B-18	Sequence 18, Appl
8	5	8.6	10	1 US-08-243-839C-135	Sequence 135, Appl
9	5	8.6	10	2 US-09-648-40A-18	Sequence 18, Appl
10	5	8.6	10	2 US-09-839-329-4	Sequence 4, Appl
11	5	8.6	10	2 US-10-421-18	Sequence 18, Appl
12	5	8.6	10	2 US-10-077-61-9	Sequence 3, Appl
13	5	8.6	10	4 PCT-US96-01733-4	Sequence 4, Appl
14	4	6.9	8	1 US-08-441-818-262	Sequence 6, Appl
15	4	6.9	8	1 US-08-244-855-6	Sequence 6, Appl
16	4	6.9	8	1 US-08-529-190B-70	Sequence 70, Appl
17	4	6.9	8	1 US-08-529-190B-71	Sequence 71, Appl
18	4	6.9	8	1 US-08-922-267A-68	Sequence 68, Appl
19	4	6.9	8	2 US-08-601-184-6	Sequence 6, Appl
20	4	6.9	8	2 US-08-441-818-262	Sequence 262, Appl
21	4	6.9	8	2 US-08-441-818-263	Sequence 263, Appl
22	4	6.9	8	2 US-08-444-818-264	Sequence 264, Appl
23	4	6.9	8	2 US-08-496-791-8	Sequence 8, Appl
24	4	6.9	8	2 US-09-419-826-39	Sequence 39, Appl
25	4	6.9	8	2 US-08-975-614-3	Sequence 3, Appl
26	4	6.9	8	2 US-08-648-40A-10	Sequence 10, Appl
27	6.9			US-08-475-955-194	Sequence 194, App
				US-08-475-955-195	Sequence 195, App
				US-08-475-955-196	Sequence 196, App
				US-08-475-955-197	Sequence 197, App
				US-08-475-955-204	Sequence 204, App
				US-09-839-986-8	Sequence 8, Appl
				US-09-792-480-9	Sequence 9, Appl
				US-10-083-888-18	Sequence 18, Appl
				US-10-080-505-54	Sequence 54, Appl
				US-10-209-421-10	Sequence 10, Appl
				US-09-308-140-8	Sequence 8, Appl
				US-10-645-655-8	Sequence 8, Appl
				US-09-856-070-7	Sequence 7, Appl
				US-09-496-391-26	Sequence 26, Appl
				US-10-028-056-25	Sequence 25, Appl
				US-07-867-819D-139	Sequence 139, App
				US-07-867-819D-141	Sequence 141, App
				US-07-867-819D-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-621-803-221
; Sequence 221, Application US/08621803
; Patent No. 5851802

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUREMENTS: 265

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 221:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

FEATURE:
NAME/KEY: misc feature

OTHER INFORMATION: "XMP:3.82:"

NAME/KEY: modified-site
LOCATION: C-terminus

OTHER INFORMATION: /label= Amidation

OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-08-621-803-221

Query Match Best Local Similarity 8.6%; Score 5; DB 1; Length 9;

RESULT 2
 US-08-621-259A-213
 ; Sequence 213, Application US/08621259A
 ; Patent No. 5858974
 ; GENERAL INFORMATION:
 ; APPLICANT: Little II, Roger G
 ; APPLICANT: Lim, Edward
 ; APPLICANT: Fadem, Mitchell B.
 ; TITLE OF INVENTION: Anti-Fungal Peptides
 ; NUMBER OF SEQUENCES: 252
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/621,259A
 ; FILING DATE: 21-MAR-1996
 ; PRIORITY APPLICATION DATA:
 ; REFERENCE/DOCKET NUMBER: 11021US02
 ; APPLICATION NUMBER: 08/504,841
 ; FILING DATE: 20-JUL-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 213:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: "XMP.382:"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: C-Terminal
 ; OTHER INFORMATION: /label= Amideation
 ; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
 ; US-08-621-259A-213

Query Match **8.6%**; Score 5; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LQLIK 17
Db 4 LQLIK 8

RESULT 3
 US-08-159-339A-343
 ; Sequence 343, Application US/08159339A
 ; Patent No. 6037135
 ; GENERAL INFORMATION:
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Celis, Esteban
 ; TITLE OF INVENTION: HLA Binding peptides and Their
 ; NUMBER OF SEQUENCES: 1254
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA

RESULT 4
 US-08-159-339A-405
 ; Sequence 405, Application US/08159339A
 ; Patent No. 6037135
 ; GENERAL INFORMATION:
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Celis, Esteban
 ; TITLE OF INVENTION: HLA Binding peptides and Their
 ; NUMBER OF SEQUENCES: 1254
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA

FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: "XMP_382:
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION:
 OTHER INFORMATION: /label= Amidation
 /note= "The C-Terminus is Amidated."
 SEQUENCE DESCRIPTION: SEQ ID NO: 213:
 US-09-677-664B-213

Query Match 8.6%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 LQLLK 17
 Db 4 LQLLK 8

RESULT 7
 US-09-792-480-18
 Sequence 18 Application US/09792480
 ; Patent No. 6669951
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothbard, Jonathan B.
 ; APPLICANT: Wender, Paul A.
 ; APPLICANT: McGrane, P. Leo
 ; APPLICANT: Sista, Lalitha V.S.
 ; APPLICANT: Kirschberg, Thorsten A.
 ; APPLICANT: Celgate, Inc.
 ; APPLICANT: Compositions and Methods for Enhancing Drug Delivery
 ; TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
 ; FILE REFERENCE: 019801-000230US
 ; CURRENT APPLICATION NUMBER: US/09/792,480
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/150,510
 ; PRIOR FILING DATE: 1999-08-24
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 18
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:A-54
 OTHER INFORMATION: Ala-substituted analog of HIV-1 tat protein basic
 NAME/KEY: MOD_RES
 LOCATION: (1)
 OTHER INFORMATION: Xaa = fluorescein linked to amino group of
 OTHER INFORMATION: aminoheanoic acid (Fl-ahx) attached to the
 OTHER INFORMATION: N-terminal amino group of Arg
 ; US-09-792-480-18

Query Match 8.6%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 43 KKRRRA 47
 Db 2 KKRRRA 6

RESULT 8
 US-08-248-839C-135
 Sequence 135 Application US/08248839C
 ; Patent No. 5843702
 ; GENERAL INFORMATION:
 ; APPLICANT: McConnell, David
 ; APPLICANT: Devine, Kevin

APPLICANT: O'Kane, Charles
 TITLE OF INVENTION: A Gene Expression System
 NUMBER OF SEQUENCES: 185
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: 405 Lexington Avenue
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10174-6401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,839C
 FILING DATE: 25-MAY-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gregg, Valeta A.
 REGISTRATION NUMBER: 35.127
 REFERENCE/DOCKET NUMBER: 3614.214-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 135:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-248-839C-135

Query Match 8.6%; Score 5; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 34 SIMLL 38
 Db 3 SIMLL 7

RESULT 9
 US-09-648-400A-18
 Sequence 18 Application US/09648400A
 ; Patent No. 6593392
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothbard, Jonathan B.
 ; APPLICANT: Wender, Paul A.
 ; APPLICANT: McGrane, P. Leo
 ; APPLICANT: Sista, Lalitha V.S.
 ; APPLICANT: Kirschberg, Thorsten A.
 ; APPLICANT: Celgate, Inc.
 ; APPLICANT: Compositions and Methods for Enhancing Drug Delivery
 ; TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
 ; FILE REFERENCE: 019801-000210US
 ; CURRENT APPLICATION NUMBER: US/09/48,400A
 ; CURRENT FILING DATE: 2000-08-24
 ; PRIOR FILING DATE: 1999-08-24
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 18
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:A-54
 OTHER INFORMATION: Ala-substituted analog of HIV-1 tat protein basic
 OTHER INFORMATION: region Tat-49-57
 FEATURE:

; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = fluorescein linked to amino group of
; OTHER INFORMATION: aminohexanoic acid (Fl-ahx)
; US-09-648-400A-18

Query Match 8.6%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 KKRRA 47
Db 3 KKRRA 7

RESULT 10
US-09-839-329-4
; Sequence 4, Application US/09839329
Patent No. 6664940
GENERAL INFORMATION:
APPLICANT: Michael P. Sherman
APPLICANT: Warner C. Greene
APPLICANT: Carlos M.C. de No. 6664040ohnra
APPLICANT: Ulrich Schubert
APPLICANT: Peter Heuklein
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
TITLE OF INVENTION: A MOLECULE INTO A CELL
FILE REFERENCE: G&C 30448.91-US-U2
CURRENT APPLICATION NUMBER: US/09/839,329
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/206,610
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/267,827
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human immunodeficiency virus
US-09-839-329-4

Query Match 8.6%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GKRR 46
Db 2 GKRR 6

RESULT 11
US-10-203-421-18
; Sequence 18, Application US/10209421
Patent No. 6759387
GENERAL INFORMATION:
APPLICANT: Rothbard, Jonathan B.
APPLICANT: Wender, Paul A.
APPLICANT: McGrane, F. Leo
APPLICANT: Sista, Lalitha V.S.
APPLICANT: Kirchberg, Thorsten A.
APPLICANT: CellGate, Inc.
TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
TITLE OF INVENTION: Across and Into Epithelial Tissues
FILE REFERENCE: 019801-00021IUS
CURRENT APPLICATION NUMBER: US/10/209,421
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 60/150,510
PRIOR FILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: US 09/648,400
PRIOR FILING DATE: 2000-08-24

Query Match 8.6%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GKRR 46
Db 2 GKRR 6

RESULT 12
US-10-007-761-9
; Sequence 9, Application US/10007761
; Patent No. 6855693
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Peptides for Activation and Inhibition
TITLE OF INVENTION: Of delta-PKC
FILE REFERENCE: 5800-8208 US00
CURRENT APPLICATION NUMBER: US/10/007,761
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/262,060
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tat-derived carrier peptide
US-10-007-761-9

Query Match 8.6%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GKRR 46
Db 2 GKRR 6

RESULT 13
PC-TUS96-01735-4
; Sequence 4, Application PC/TUS9601735
GENERAL INFORMATION:
APPLICANT: Marks, Andrew R.
TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQ ID NOS: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10112-0228

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/01735
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/386, 039
 FILING DATE: 09-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kole, Lisa B
 REGISTRATION NUMBER: 35,225
 REFERENCE/DOCKET NUMBER: A30042 - 165/30555
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-408-2828
 TELEFAX: 212-765-2519
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 STRANDEDNESS: single
 MOLECULE TYPE: peptide
 TOPOLOGY: linear
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 FEATURE:
 PCT-US96-01735-4

Query Match 8.6%; Score 5; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Qy 12 FLQQL 16
 Db 4 FLQQL 8

RESULT 14
 US-08-037-579A-6
 Sequence 6, Application US/08037579A
 Patent No. 5552537
 GENERAL INFORMATION:
 APPLICANT: Zhang, Ke
 APPLICANT: Max, Edward E
 APPLICANT: Saxon, Andrew
 TITLE OF INVENTION: IGE ISOFORMS AND METHODS OF USE
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HORVATH, TEST, ALBRITTON & HERBERT
 STREET: 8TH FLOOR, 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244, 855
 FILING DATE: 16-JUN-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Milchard, Leonard C.
 REGISTRATION NUMBER: 29,009
 RREFERENCE/DOCKET NUMBER: 604-285
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4005
 TELEFAX: (703) 816-1100
 TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: peptide
 US-08-244-855-6

Query Match 6.9%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Qy 45 RRAT 48
 Db 2 RRAT 5

Wed Dec 14 08:46:43 2005

us-10-031-158b-14.oliszlm.rai

Page 7

Job time : 47 secs

THIS PAGE BLANK (USPTO)

Copyright (c) 1993 - 2005 Compugen Ltd.

Gentcore version 5.1.6

Om protein - protein search, using sw model
Run on: December 13, 2005, 08:25:42 ; Search time 159 Seconds
Sequence: (without alignments)
Scoring table: OLIGO

Title: US-10-031-158B-14

Perfect score: 58

Sequence: 1 MQMFPPSPPLFPLQLIKQSS.....RYIGKRRATRFWDDPRRGTP 58

152.416 Million cell updates/sec

Searched: 1867569 seqs, 417829326 residues
Word size : 0

Total number of hits satisfying chosen parameters: 151674

Minimum DB seq length: 8

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published Applications AA_Main.*

1: /ccn2_6/ptodata/1/pupbaa/US07_PUBCOMB.pep: *
2: /ccn2_6/ptodata/1/pupbaa/US09_PUBCOMB.pep: *
3: /ccn2_6/ptodata/1/pupbaa/US10A_PUBCOMB.pep: *
4: /ccn2_6/ptodata/1/pupbaa/US10B_PUBCOMB.pep: *
5: /ccn2_6/ptodata/1/pupbaa/US11_PUBCOMB.pep: *
6: /ccn2_6/ptodata/1/pupbaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5	8	4	US-10-137-867-292
2	5	8	4	Sequence 292, App
3	5	8	4	Sequence 221, App
4	5	8	3	US-09-792-480-18
5	5	9	3	US-09-870-216C-3
5	5	8	4	US-10-017-327-3
6	5	9	4	US-10-144-188-2
7	5	8	6	US-09-839-329-4
8	5	10	3	US-09-572-404B-238
9	5	8	6	US-09-572-404B-144
10	5	8	6	US-09-572-404B-3212
11	5	8	6	US-10-007-761-9
12	5	8	6	US-10-083-960-18
13	5	8	6	US-10-209-421-18
14	5	8	6	US-10-168-789A-26
15	5	8	6	US-10-168-789A-27
16	5	8	6	US-10-421-548-7
17	5	8	6	US-10-421-503-65
18	5	8	6	US-10-843-731-9
19	5	8	6	US-10-936-237-47
20	5	10	5	US-10-513-003-65
21	4	6	8	US-09-815-837-14
22	4	6	9	US-09-804-682-170
23	4	6	9	US-09-792-480-9
24	4	6	9	US-09-756-875-10
25	4	6	9	US-09-756-875-11
26	4	6	9	US-09-756-875-20
27	4	6	9	US-09-756-875-21

ALIGNMENTS

RESULT 1	US-10-137-867-292	US-10-137-867-292	Sequence 22, Appl
		; Sequence 292, Application US/10137867	Sequence 23, Appl
		; Publication No. US20030207349A1	Sequence 24, Appl
		; GENERAL INFORMATION:	Sequence 29, Appl
		; APPLICANT: Baker, Kevin P.	Sequence 7, Appl
		; APPLICANT: Beresini, Maureen	Sequence 19, Appl
		; APPLICANT: DeForge, Laura	Sequence 8, Appl
		; APPLICANT: Desnoyers, Luc	Sequence 76, Appl
		; APPLICANT: Filvaroff, Ellen	Sequence 17, Appl
		; APPLICANT: Gao, Wei-Qiang	Sequence 244, Appl
		; APPLICANT: Gerritzen, Mary E.	Sequence 15, Appl
		; APPLICANT: Godowski, Paul J.	Sequence 353, APP
		; APPLICANT: Gurney, Austin L.	Sequence 408, APP
		; APPLICANT: Sherwood, Steven	Sequence 417, APP
		; APPLICANT: Smith, Victoria	Sequence 419, APP
		; APPLICANT: Stewart, Timothy A.	Sequence 10, Appl
		; APPLICANT: Tumas, Daniel	Sequence 25, Appl
		; APPLICANT: Watanabe, Colin K	
		; APPLICANT: Wood, William	
		; APPLICANT: Zhang, Zemin	
		; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEARIC ACIDS ENCODING THE SAME	
		; TITLE OF INVENTION: ACIDS ENCODING THE SAME	
		; FILE REFERENCE: P3130R1C146	
		; CURRENT APPLICATION NUMBER: US/10/137,867	
		; CURRENT FILING DATE: 2002-05-03	
		; PRIOR APPLICATION REMOVED - See Palm or File Wrapper	
		; NUMBER OF SEQ ID NOS: 550	
		; SEQ ID NO: 292	
		; LENGTH: 428	
		; TYPE: RTT	
		; ORGANISM: Homo Sapien	
		US-10-137-867-292	

Query	Match	Similarity	8.6%	Score	5	DB	4	Length	8
Matches	5	Conservative	0	Pred.	No.	1.7e+05	;	Mismatches	0
OY	9	LFFFL	13					Indels	0
Db	1	LFFFL	5					Gaps	0

RESULT 2	US-09-755-527-221	US-09-755-527-221	Sequence 22, Appl
		; Sequence 221, Application US/09765527	Sequence 23, Appl
		; PATENT NO. US2002006638A1	Sequence 24, Appl
		; GENERAL INFORMATION:	Sequence 29, Appl
		; APPLICANT: Better, Marc D.	Sequence 7, Appl

TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTY: United States of America

ZIP: 60605-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MC-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,527

FILING DATE: 18-Jan-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/621,803

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/74-6300
TELEX: 25-3856
FAX: 312/474-0448

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: "Xmp_382:"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminal

OTHER INFORMATION: /label= Amidation

/note= "The C-Terminus is Amidated."

SEQUENCE DESCRIPTION: SEQ ID NO: 221;

65-527-221.

Match 8.6%; Score 5; DB 3; Length 9;
Local Similarity 100.0%; Pred. No. 1.7e+06;
5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 LQQLK 17
| | | |
4 LQLK 8

3

192-480-18
ince 18, Application US/09792480
t No. US20020127198A1

AL INFORMATION:

ICANT: Rohrhard, Jonathan B.

ICANT: Wender, Paul A.

ICANT: McGrane, P. Leo

ICANT: Sista, Lalitha V.S.

ICANT: Kirscherberg, Thorsten A.

ICANT: CellGate, Inc.

NAME OF INVENTION: Compositions and Methods for Enhancing Drug Delivery

NAME OF INVENTION: Across and Into Epithelial Tissues

, REFERENCE: 019801-000230US
, REFERENCE NUMBER: US/09/792,480
ENT APPLICATION NUMBER: US/09/792,480
ENT FILING DATE: 2001-02-23
ENT APPLICATION NUMBER: US 09/648,400
ENT FILING DATE: 2000-08-24

RESULT 4

US-09-870-216C-3

; Sequence 3, Application US/09870216C
; Publication No. US20040138135A1

; GENERAL INFORMATION:

; APPLICANT: Charles A. Nicolette

; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER

; FILE REFERENCE: 6812688121010

; CURRENT APPLICATION NUMBER: US/09/870,216C

; CURRENT FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: 60/209,391

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: 60/226,256

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/257,008

; PRIOR FILING DATE: 2000-12-20

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-870-216C-3

RESULT 5

US-10-017-327-3

; Sequence 3, Application US/10017327

; Publication No. US20020155471A1

; GENERAL INFORMATION:

; APPLICANT: Charles A. Nicolette

; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS AND METHODS FOR USING SAME

; TITLE OF INVENTION: METHODS FOR USING SAME

; FILE REFERENCE: GZ_2101.20

; CURRENT APPLICATION NUMBER: US/10/017,327

; CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-17-327-3

Query Match 8.6%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 FLOL 16
Db 1 FLOLL 5

RESULT 6
US-10-144-188-2
Sequence 2, Application US/10144188
Publication No. US20030170212A1
GENERAL INFORMATION:
APPLICANT: Cai, Zeling
APPLICANT: Jackson, Michael R.
APPLICANT: Peterson, Per A.
APPLICANT: Shi, Weixing
APPLICANT: Kong, Yan
APPLICANT: Degraw, Juli
TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific To Treat Autoimmune And A
FILE REFERENCE: For No. US20030170212A1-Tumor Antigens To Treat Autoimmune And A
CURRENT APPLICATION NUMBER: US/10/144,188
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/291,300
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide antigen
US-10-144-188-2

Query Match 8.6%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PPSP 9
Db 2 PPSP 6

RESULT 7
US-09-839-329-4
Sequence 4, Application US/09839329
Publication No. US20020020207A1
GENERAL INFORMATION:
APPLICANT: Michael P. Sherman
APPLICANT: Warner C. Greene
APPLICANT: Carlos M. C. de No. 6664040chna
APPLICANT: Ulrich Schubert
APPLICANT: Peter Henklein
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF
TITLE OF INVENTION: A MOLECULE INTO A CELL
FILE REFERENCE: G&C 30448.91-US-U2
CURRENT APPLICATION NUMBER: US/09/839,329
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/206,610
PRIOR APPLICATION NUMBER: 60/267,827
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 5

Query Match 8.6%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 42 GKRR 46
Db 2 GKRR 6

RESULT 8
US-09-572-404B-238
Sequence 238, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 238
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in MTNR1B at 351-360 and may interact with Sequer
US-09-572-404B-238

Query Match 8.6%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 SRRL 24
Db 1 SRRL 5

RESULT 9
US-09-572-404B-144
Sequence 144, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 144
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in NTAK at 681-690 and may interact with Sequence
US-09-572-404B-144

Query Match 8.6%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 PRRGT 57
Db 6 PRRGT 10

RESULT 10
US-09-572-404B-3212
Sequence 3212, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3212
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens

FEATURE:
OTHER INFORMATION: sequence located in HOXA9 OR HOX1G at 369-378 and may interact w1
OTHER INFORMATION: Sequence 3211 in this patent.

Query Match 8.6%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 RKRATR 49
Db 4 RKRATR 8

RESULT 11
US-10-007-761-9
Sequence 9, Application US/10007761
Publication No. US20020150984A1
GENERAL INFORMATION:
APPLICANT: MOCHLY-ROSEN, Daria
TITLE OF INVENTION: Peptides for Activation and Inhibition
FILE REFERENCE: Of delta-PCC
CURRENT APPLICATION NUMBER: US/10/007,761
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/262,060
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Tat-derived carrier peptide
US-10-007-761-9

Query Match 8.6%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 KKARRA 47
Db 3 KKARRA 7

RESULT 13
US-10-209-421-18
Sequence 18, Application US/10209421
Publication No. US20030083256A1
GENERAL INFORMATION:
APPLICANT: Rothbard, Jonathan B.
APPLICANT: Wender, Paul A.
APPLICANT: McGrane, P. Leo
APPLICANT: Sista, Lalitha V.S.
APPLICANT: Kirchberg, Thorsten A.
APPLICANT: CellGate, Inc.
TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
FILE REFERENCE: 019801-000211US
CURRENT APPLICATION NUMBER: US/10/209,421
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 60/150,510
PRIOR FILING DATE: 1999-05-24
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:A-54
OTHER INFORMATION: Ala substituted analog of HIV-1 tat protein basic
FEATURE:
NAME/KEY: MOD_RBS
LOCATION: (1)

RESULT 12
US-10-083-960-18
Sequence 18, Application US/10083960
Publication No. US20030022831A1
GENERAL INFORMATION:
APPLICANT: Rothbard, Jonathan B.

```

; OTHER INFORMATION: Xaa = fluorescein linked to amino group of
; OTHER INFORMATION: amniohexanoic acid (Fl-ahx)
; US-10-209-421-18

Query Match          8.6%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Score 5; DB 4; Length 10;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      43 KKRRA 47
Db      3 KKRRA 7

RESULT 14
US-10-168-789A-26
; Sequence 26, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: INATOMI, No. US20030148943A1
; TITLE OF INVENTION: No. US20030148943A1 L- tachykinin-like Polypeptides and Use Thereof
; CURRENT APPLICATION NUMBER: US/10/168, 789A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/JP00/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-162638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
; US-10-168-789A-26

RESULT 15
US-10-168-789A-27
; Sequence 27, Application US/10168789A
; Publication No. US20030148943A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Yasuaki
; APPLICANT: NISHI, Kazunori
; APPLICANT: KITADA, Chieko
; APPLICANT: INATOMI, No. US20030148943A1
; TITLE OF INVENTION: No. US20030148943A1 L-Tachykinin-like Polypeptides and Use Thereof
; FILE REFERENCE: 2600USP
; CURRENT APPLICATION NUMBER: US/10/168, 789A
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/JPO/09083
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: JP 11-362638
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: JP 12-066714
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 27
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Polypeptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (01): (01)
; OTHER INFORMATION: Xaa means pyroglutamic acid
; US-10-168-789A-27

Query Match          8.6%; Score 5; DB 4; Length 10;
Best Local Similarity 100.0%; Score 5; DB 4; Length 10;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 LEHTF 27
Db      2 LEHTF 6

Search completed: December 13, 2005, 08:39:30
Job time : 160 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
 Run on: December 13, 2005, 08:26:32 ; Search time 11 Seconds
 Scoring table: OLIGO

Title: US-10-031-158B-14
 Perfect score: 58
 Sequence: 1 MQWRRPSPLRFQLIKQSS.....RYIGKKRRAFRWMDPRRGTP 58
 Gapop 60.0 , Gapext 60.0

Searched: 32527 seqs, 5584426 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3786
 Minimum DB seq length: 8
 Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published Applications AA_New/*
 1: /cgn2_6/ptodata/2/pubpaa/us09_NEW_PUB.pep:/*
 2: /cgn2_6/ptodata/2/pubpaa/us06_NEW_PUB.pep:/*
 3: /cgn2_6/ptodata/2/pubpaa/us07_NEW_PUB.pep:/*
 4: /cgn2_6/ptodata/2/pubpaa/us08_NEW_PUB.pep:/*
 5: /cgn2_6/ptodata/2/pubpaa/RC07_NEW_PUB.pep:/*
 6: /cgn2_6/ptodata/2/pubpaa/us10_NEW_PUB.pep:/*
 7: /cgn2_6/ptodata/2/pubpaa/us11_NEW_PUB.pep:/*
 8: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	5	8.6	10	US-11-119-098-8 Sequence 8, Appli Sequence 26, Appli Sequence 15, Appli Sequence 16, Appli Sequence 1, Appli Sequence 14, Appli Sequence 144, Appli Sequence 1, Appli Sequence 28, Appli Sequence 1, Appli Sequence 53, Appli Sequence 446, Appli RESULT 2 US-10-914-842A-26 US-10-914-842A-26 ; Sequence 25, Application US/10914842A ; Publication No. US10050260730A1 ; GENERAL INFORMATION: ; APPLICANT: Fischer, Peter Martin ; TITLE OF INVENTION: CDK2/CYCLIN A CRYSTALS AND USES THEREOF ; FILE REFERENCE: CCI-032 ; CURRENT APPLICATION NUMBER: US/10/914-842A ; CURRENT FILING DATE: 2004-08-10 ; CURRENT FILING DATE: 2004-08-10 ; PRIORITY APPLICATION NUMBER: UK 0324465.4 ; PRIORITY FILING DATE: 2003-10-20 ; NUMBER OF SEQ ID NOS: 31 ; SOFTWARE: Patentin Ver. 3.2 ; SEQ ID NO 26 ; LENGTH: 8
2	4	6.9	8	US-10-914-842A-26 Sequence 511, Appli Sequence 1, Appli Sequence 22, Appli Sequence 6, Appli Sequence 7372, Appli Sequence 511, Appli Sequence 446, Appli Sequence 511, Appli Sequence 511, Appli Sequence 8769, Appli Sequence 8797, Appli Sequence 17, Appli Sequence 5, Appli Sequence 14, Appli Sequence 208, Appli
3	4	6.9	10	US-11-096-706-208 US-10-467-657-8729 US-10-467-657-8769 US-10-467-657-8797 US-10-914-842A-17 US-10-416-0417-5 US-11-082-251-14 US-11-096-706-208
4	6.9	9	4	
5	6.9	9	6	
6	6.9	9	6	
7	6.9	10	7	
8	6.9	10	7	
9	6.9	10	7	
10	6.9	10	7	
11	6.9	10	7	
12	6.9	10	7	
13	6.9	10	7	
14	6.9	10	7	
15	6.9	10	7	
16	5.2	6	6	
17	5.2	8	6	
18	5.2	8	6	
19	5.2	8	6	
20	5.2	8	6	
21	5.2	8	6	
22	5.2	8	6	
23	5.2	8	6	
24	5.2	8	7	
25	5.2	8	7	

ALIGNMENTS

RESULT	1
US-11-119-098-8	; Sequence 8, Application US/1119098 ; Publication No. US0050267030A1 ; GENERAL INFORMATION: ; APPLICANT: Ibaao, Philip S. ; TITLE OF INVENTION: Use of deltaPKC Peptides for Modulation of Reactive Oxygen Species ; FILE REFERENCE: 56600-8213.US00 ; CURRENT APPLICATION NUMBER: US/11/119.098 ; CURRENT FILING DATE: 2005-04-29 ; PRIORITY APPLICATION NUMBER: US 60/567,315 ; PRIORITY FILING DATE: 2004-04-30 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 8 ; LENGTH: 10 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; OTHER INFORMATION: Tat-derived carrier peptide US-11-119-098-8
Query	Match Best Local Similarity 100.0%; Score 5; DB 7; Length 10; Matches 5; Conservancy 0; Mismatches 0; Indels 0; Gaps 0;
Ov	42 GKRR 46 Db 2 GKRR 6

Sequence 17, Appli
Sequence 24, Appli
Sequence 32, Appli
Sequence 3141, Appli
Sequence 3214, Appli
Sequence 98, Appli
Sequence 152, Appli
Sequence 213, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 26, Appli
Sequence 10, Appli
Sequence 44, Appli
Sequence 9002, Appli

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-914-842A-26

Query Match      6.9%; Score 4; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY        44 KRRRA 47
Db         3 KRRRA 6

RESULT 3
US-10-499-715-15
; Sequence 15, Application US/10499715
; Publication No. US20050250717A1
; GENERAL INFORMATION:
; APPLICANT: BENAYAHU, Dafna
; TITLE OF INVENTION: CHROMATIN REMODELING PROTEIN AS A MARKER EXPRESSED BY STROMAL PRO
; TITLE OF INVENTION: CELLS, DNA ENCODING SAME, ANTIBODIES THERETO, AND METHODS OF USE
; FILE REFERENCE: BENAYAHU-1, PCT
; CURRENT APPLICATION NUMBER: US10/499,715
; CURRENT FILING DATE: 2004-06-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-499-715-15

Query Match      6.9%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY        43 KKRR 46
Db         1 KKRR 4

RESULT 4
US-10-499-715-16
; Sequence 16, Application US/10499715
; Publication No. US20050250717A1
; GENERAL INFORMATION:
; APPLICANT: BENAYAHU, Dafna
; APPLICANT: SHUR, Irina
; TITLE OF INVENTION: CHROMATIN REMODELING PROTEIN AS A MARKER EXPRESSED BY STROMAL PRO
; TITLE OF INVENTION: CELLS, DNA ENCODING SAME, ANTIBODIES THERETO, AND METHODS OF USE
; FILE REFERENCE: BENAYAHU-1, PCT
; CURRENT APPLICATION NUMBER: US10/499,715
; CURRENT FILING DATE: 2004-06-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-499-715-16

Query Match      6.9%; Score 4; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY        43 KKRR 46
Db         1 KKRR 4

RESULT 5
US-11-76-868-1
; Sequence 1, Application US/11176868
; Publication No. US20050245454A1
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; TITLE OF INVENTION: Methods and Compositions for Impairing Multiplication of HIV-1
; FILE REFERENCE: GGR3USA
; CURRENT APPLICATION NUMBER: US/11/176,868
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/10/323,013
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/10/114,176
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-76-868-1

Query Match      6.9%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY        43 KKRR 46
Db         2 KKRR 5

RESULT 6
US-11-037-864-144
; Sequence 144, Application US/11097864
; Publication No. US2005025924A1
; GENERAL INFORMATION:
; APPLICANT: Chalilte-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEAR ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: RT
; ORGANISM: Homo Sapien
US-11-037-864-144

Query Match      6.9%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY        32 NFSL 35
Db         6 NFSL 9

RESULT 7
US-11-097-912-144
; Sequence 144, Application US/11097912
; Publication No. US2005026592A1

```

GENERAL INFORMATION:
 APPLICANT: Challita-Eid, Pia M.
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Paris, Mary
 APPLICANT: Hubert, Rene S.
 APPLICANT: Morrison, Karen Jane Meyrick
 APPLICANT: Jakobovits, Ayala
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
 FILE REFERENCE: CL-1849 US NA
 CURRENT APPLICATION NUMBER: US/11/152,747
 CURRENT FILING DATE: 2005-06-14
 PRIOR APPLICATION NUMBER:
 PRIOR FILING DATE:
 NUMBER OF SEQ ID NOS: 47
 SEQ ID NO 144
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo Sapien
 RS-11-097-912-144
 RESULT 8
 Query Match 6.9%; Score 4; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Mirus Corporation
 APPLICANT: Rozema, David
 APPLICANT: Wolff, Jon
 APPLICANT: Wakefield, Darren
 APPLICANT: Ekena, Kirk
 APPLICANT: Haggstrom, James
 TITLE OF INVENTION: Reversible Modification of Membrane Interaction
 FILE REFERENCE: Mirus 035.01
 CURRENT APPLICATION NUMBER: US/10/444,662
 CURRENT FILING DATE: 2003-05-23
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 RS-11-152-747-28
 RESULT 9
 Query Match 6.9%; Score 4; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: E. I. du Pont de Nemours, Inc.
 APPLICANT: Cheng, Qiong
 APPLICANT: Tao, Juan
 RS-11-032-794-53
 RESULT 10
 Query Match 6.9%; Score 4; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: FRANZOZO, GUIDO
 APPLICANT: PAPA, SALVATORE
 APPLICANT: BUBICI, CONCETTA
 APPLICANT: DESMABLE, ENRICO
 APPLICANT: ZAZZERONI, FRANCESCA
 TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
 CELL DEATH OR APOPTOSIS BY TARGETING JNK
 FILE REFERENCE: 21459-97816
 CURRENT APPLICATION NUMBER: US/11/032,794
 CURRENT FILING DATE: 2005-01-10
 PRIOR APPLICATION NUMBER: 11/000,365
 PRIOR FILING DATE: 2004-11-29
 PRIOR APPLICATION NUMBER: 60/526,231
 PRIOR FILING DATE: 2003-12-02
 PRIOR APPLICATION NUMBER: 10/626,905
 PRIOR FILING DATE: 2003-07-25
 PRIOR APPLICATION NUMBER: 10/263,330
 PRIOR FILING DATE: 2002-10-02
 PRIOR APPLICATION NUMBER: 60/328,811
 PRIOR FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/326,492
 PRIOR FILING DATE: 2001-10-02
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: Patentin Ver. 3.3
 SEQ ID NO 53
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 RS-11-097-964-446
 RESULT 11
 Query Match 6.9%; Score 4; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GENERAL INFORMATION:
 APPLICANT: Challita-Eid, Pia M.

```

; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary S.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-446

Query Match      6.9%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      32 NFSL 35
Db      7 NFSL 10

RESULT 12
US-11-097-864-511
; Sequence 511, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 511
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-511

Query Match      6.9%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      32 NFSL 35
Db      7 NFSL 10

RESULT 13
US-11-097-912-446
; Sequence 446, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challitt-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary S.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-446

Query Match      6.9%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      32 NFSL 35
Db      7 NFSL 10

RESULT 14
US-11-097-912-511
; Sequence 511, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challitt-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 511
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-511

Query Match      6.9%; Score 4; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      32 NFSL 35
Db      7 NFSL 10

```

; GENERAL INFORMATION:
; APPLICANT: Mirus Bio
; APPLICANT: Monahan, Sean
; APPLICANT: Nader, Lisa
; TITLE OF INVENTION: Polymerized Formamides for Use in Delivery of Compounds to Cells
; FILE REFERENCE: Mirus.044.01
; CURRENT APPLICATION NUMBER: US/11/102,432
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-102-432-1

Query Match 6.9%; Score 4; DB 7; length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Qy 43 KKRR 46
Db 3 KKRR 6

Search completed: December 13, 2005, 08:39:48
Job time : 12 secs

THIS PAGE BLANK (USPTO)